

Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val  
     -50                  -45                  -40  
 Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser  
     -35                  -30                  -25  
 Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro  
     -20                  -15                  -10                  -5  
 Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly  
     1                  5                  10  
 Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His  
     15                  20                  25  
 Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu  
     30                  35                  40  
 Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys  
     45                  50                  55                  60  
 Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe  
     65                  70                  75  
 Arg Glu Asn Val Leu Arg Asn Leu Ala Asp Lys Ala Phe Asp Arg Pro  
     80                  85                  90  
 Ile Cys Glu Ala Leu Leu Asp Gln Arg Phe Phe Asn Gly Ile Gly Asn  
     95                  100                  105  
 Tyr Leu Arg Ala Glu Ile Leu Tyr Arg Leu Lys Ile Pro Pro Phe Glu  
     110                  115                  120  
 Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln His Arg Pro Ser Pro  
     125                  130                  135                  140  
 Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Ser Asp  
     145                  150                  155  
 Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly  
     160                  165                  170  
 Glu Ala Lys Asp Gly Ser Asn Leu Cys Phe Ser Lys  
     175                  180

<210> 171  
 <211> 350  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -68...1

<400> 171  
 Met Pro Glu Gly Pro Glu Leu His Leu Ala Ser Gln Phe Val Asn Glu  
     -65                  -60                  -55  
 Ala Cys Arg Ala Leu Val Phe Gly Gly Cys Val Glu Lys Ser Ser Val  
     -50                  -45                  -40  
 Ser Arg Asn Pro Glu Val Pro Phe Glu Ser Ser Ala Tyr Arg Ile Ser  
     -35                  -30                  -25  
 Ala Ser Ala Arg Gly Lys Glu Leu Arg Leu Ile Leu Ser Pro Leu Pro  
     -20                  -15                  -10                  -5  
 Gly Ala Gln Pro Gln Gln Glu Pro Leu Ala Leu Val Phe Arg Phe Gly  
     1                  5                  10  
 Met Ser Gly Ser Phe Gln Leu Val Pro Arg Glu Glu Leu Pro Arg His  
     15                  20                  25  
 Ala His Leu Arg Phe Tyr Thr Ala Pro Pro Gly Pro Arg Leu Ala Leu  
     30                  35                  40  
 Cys Phe Val Asp Ile Arg Arg Phe Gly Arg Trp Asp Leu Gly Gly Lys  
     45                  50                  55                  60  
 Trp Gln Pro Gly Arg Gly Pro Cys Val Leu Gln Glu Tyr Gln Gln Phe  
     65                  70                  75  
 Arg Leu Lys Ile Pro Pro Phe Glu Lys Ala Arg Ser Val Leu Glu Ala

80	85	90
Leu Gln Gln His Arg Pro Ser Pro	Glu Leu Thr Leu Ser Gln Lys Ile	
95	100	105
Arg Thr Lys Leu Gln Asn Pro Asp	Leu Leu Glu Leu Cys His Ser Val	
110	115	120
Pro Lys Glu Val Asp Gln Leu Gly	Gly Arg Gly Tyr Gly Ser Glu Ser	
125	130	135
Gly Glu Glu Asp Phe Ala Ala Phe	Arg Ala Trp Leu Arg Cys Tyr Gly	
145	150	155
Met Pro Gly Met Ser Ser Leu Gln	Asp Arg His Gly Arg Thr Ile Trp	
160	165	170
Phe Gln Gly Asp Pro Gly Pro	Leu Ala Pro Lys Gly Arg Lys Ser Arg	
175	180	185
Lys Lys Lys Ser Lys Ala Thr Gln	Leu Ser Pro Glu Asp Arg Val Glu	
190	195	200
Asp Ala Leu Pro Pro Ser Lys Ala	Pro Ser Lys Thr Arg Arg Ala Lys	
205	210	215
Arg Asp Leu Pro Lys Arg Thr Ala	Thr Gln Arg Pro Glu Gly Thr Ser	
225	230	235
Leu Gln Gln Asp Pro Glu Ala Pro	Thr Val Pro Lys Lys Gly Arg Arg	
240	245	250
Lys Gly Arg Gln Ala Ala Ser Gly	His Cys Arg Pro Arg Lys Val Lys	
255	260	265
Ala Asp Ile Pro Ser Leu Glu	Pro Glu Gly Thr Ser Ala Ser	
270	275	280

&lt;210&gt; 172

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -68...-1

&lt;400&gt; 172

Met Pro Glu Gly Pro Glu Leu His	Leu Ala Ser Gln Phe Val Asn Glu	
-65	-60	-55
Ala Cys Arg Ala Leu Val Phe	Gly Gly Cys Val Glu Lys Ser Ser Val	
-50	-45	-40
Ser Arg Asn Pro Glu Val Pro	Phe Glu Ser Ser Ala Tyr Arg Ile Ser	
-35	-30	-25
Ala Ser Ala Arg Gly Lys Glu	Leu Arg Leu Ile Leu Ser Pro Leu Pro	
-20	-15	-10
Gly Ala Gln Pro Gln Gln Glu	Pro Leu Ala Leu Val Phe Arg Phe Gly	
1	5	10
Met Ser Gly Ser Phe Gln Leu	Val Pro Arg Glu Glu Leu Pro Arg His	
15	20	25
Ala His Leu Arg Phe Tyr Thr	Ala Pro Pro Gly Pro Arg Leu Ala Leu	
30	35	40
Cys Phe Val Asp Ile Arg Arg	Phe Gly Arg Trp Asp Leu Gly Gly Lys	
45	50	55
Trp Gln Pro Gly Arg Gly Pro	Cys Val Leu Gln Glu Tyr Gln Gln Phe	
65	70	75
Arg Glu Asn Val Leu Arg Asn	Leu Ala Asp Lys Ala Phe Asp Arg Pro	
80	85	90
Ile Cys Glu Ala Leu Leu Asp	Gln Arg Phe Phe Asn Gly Ile Gly Asn	
95	100	105
Tyr Leu Arg Ala Glu Ile Leu	Tyr Arg Leu Lys Ile Pro Pro Phe Glu	
110	115	120

Lys Ala Arg Ser Val Leu Glu Ala Leu Gln Gln 118 Arg Pro Ser Pro  
 125 130 135 140  
 Glu Leu Thr Leu Ser Gln Lys Ile Arg Thr Lys Leu Gln Asn Pro Asp  
 145 150 155  
 Leu Leu Glu Leu Cys His Ser Val Pro Lys Glu Val Val Gln Leu Gly  
 160 165 170  
 Gly Arg Gly Tyr Gly Ser Glu Ser Gly Glu Glu Asp Phe Ala Ala Phe  
 175 180 185  
 Arg Ala Trp Leu Arg Cys Tyr Gly Met Pro Gly Met Ser Ser Leu Gln  
 190 195 200  
 Asp Arg His Gly Arg Thr Ile Trp Phe Gln Gly Asp Pro Gly Pro Leu  
 205 210 215 220  
 Ala Pro Lys Gly Arg Lys Ser Arg Lys Lys Ser Lys Ala Thr Gln  
 225 230 235  
 Leu Ser Pro Glu Asp Arg Val Glu Asp Ala Leu Pro Pro Ser Lys Ala  
 240 245 250  
 Pro Ser Arg Thr Arg Arg Ala Lys Arg Asp Leu Pro Lys Arg Thr Ala  
 255 260 265  
 Thr Gln Arg Pro Glu Gly Thr Ser Leu Gln Gln Asp Pro Glu Ala Pro  
 270 275 280  
 Thr Val Pro Lys Lys Gly Arg Arg Lys Gly Arg Gln Ala Ala Ser Gly  
 285 290 295 300  
 His Cys Arg Pro Arg Lys Val Lys Ala Asp Ile Pro Ser Leu Glu Pro  
 305 310 315  
 Glu Gly Thr Ser Ala Ser  
 320

<210> 173  
 <211> 190  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -82...-1

<400> 173  
 Met Tyr Val Trp Pro Cys Ala Val Val Leu Ala Gln Tyr Leu Trp Phe  
 -80 -75 -70  
 His Arg Arg Ser Leu Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala Gly  
 -65 -60 -55  
 Val Ser Leu Pro Gly Ile Leu Thr Ala Lys Cys Gly Ala Glu Val Ile  
 -50 -45 -40 -35  
 Leu Ser Asp Ser Ser Glu Leu Pro His Cys Leu Glu Val Cys Arg Gln  
 -30 -25 -20  
 Ser Cys Gln Met Asn Asn Leu Pro His Leu Gln Val Val Gly Leu Thr  
 -15 -10 -5  
 Trp Gly His Ile Ser Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp Ile  
 1 5 10  
 Ile Leu Ala Ser Asp Val Phe Phe Glu Pro Glu Asp Phe Glu Asp Ile  
 15 20 25 30  
 Leu Ala Thr Ile Tyr Phe Leu Met His Lys Asn Pro Lys Val Gln Leu  
 35 40 45  
 Trp Ser Thr Tyr Gln Val Arg Ser Ala Asp Trp Ser Leu Glu Ala Leu  
 50 55 60  
 Leu Tyr Lys Trp Asp Met Lys Cys Val His Ile Pro Leu Glu Ser Phe  
 65 70 75  
 Asp Ala Asp Lys Glu Asp Ile Ala Glu Ser Thr Leu Pro Gly Arg His  
 80 85 90  
 Thr Val Glu Met Leu Val Ile Ser Phe Ala Lys Asp Ser Leu

95

100

105

<210> 174  
<211> 285  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -232..-1

<400> 174  
Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Arg Ile Phe Lys Ile  
-230 -225 -220  
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu  
-215 -210 -205  
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg  
-200 -195 -190 -185  
Val His Leu Met Gly Asp Asn Leu Cys Asn Asp Gly Ser Leu Leu Leu  
-180 -175 -170  
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg  
-165 -160 -155  
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val  
-150 -145 -140  
Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile  
-135 -130 -125  
Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys  
-120 -115 -110 -105  
Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Glu Glu Ile Val Phe  
-100 -95 -90  
Arg Tyr Tyr His Lys Leu Arg Met Ser Ala Glu Tyr Ser Gln Ser Trp  
-85 -80 -75  
Gly His Phe Gln Asn Arg Val Asn Leu Val Gly Asp Ile Phe Arg Asn  
-70 -65 -60  
Asp Gly Ser Ile Met Leu Gln Gly Val Arg Glu Ser Asp Gly Gly Asn  
-55 -50 -45  
Tyr Thr Cys Ser Ile His Leu Gly Asn Leu Val Phe Lys Lys Thr Ile  
-40 -35 -30 -25  
Val Leu His Val Ser Pro Glu Glu Pro Arg Thr Leu Val Thr Pro Ala  
-20 -15 -10  
Ala Leu Arg Pro Leu Val Leu Gly Gly Asn Gln Leu Val Ile Ile Val  
-5 1 5  
Gly Ile Val Cys Ala Thr Ile Leu Leu Pro Val Leu Ile Leu Ile  
10 15 20  
Val Lys Lys Thr Cys Gly Asn Lys Ser Ser Val Asn Ser Thr Val Leu  
25 30 35 40  
Val Lys Asn Thr Lys Lys Thr Asn Pro Lys Lys Lys  
45 50

<210> 175  
<211> 153  
<212> PRT  
<213> Homo sapiens

<400> 175  
Met Gly Cys Val Phe Gln Ser Thr Val Asp Lys Cys Ile Phe Lys Ile  
1 5 10 15  
Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu

20	25	30
Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg		
35	40	45
Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu		
50	55	60
Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg		
65	70	75
Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val		
85	90	95
Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu Ile		
100	105	110
Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val Thr Lys		
115	120	125
Val Glu Trp Ile Phe Ser Gly Arg Arg Ala Lys Val Thr Arg Arg Lys		
130	135	140
His His Cys Val Arg Glu Gly Ser Gly		
145	150	

&lt;210&gt; 176

&lt;211&gt; 49

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 176

Met Leu Xaa Gly Asp His Arg Ala Leu Leu Leu Lys Ile Trp Leu Leu		
1	5	10
Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val		
20	25	30
Met Glu Arg Arg Val Lys Met Thr Ser Cys Pro Ser Cys Pro Arg Phe		
35	40	45
Cys		

&lt;210&gt; 177

&lt;211&gt; 99

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -24...-1

&lt;400&gt; 177

Met Lys Ser Ala Lys Leu Gly Phe Leu Leu Arg Phe Phe Ile Phe Cys		
-20	-15	-10
Ser Leu Asn Thr Leu Leu Leu Gly Gly Val Asn Lys Ile Ala Glu Lys		
-5	1	5
Ile Cys Gly Asp Leu Lys Asp Pro Cys Lys Leu Asp Met Asn Phe Gly		
10	15	20
Ser Cys Tyr Glu Val His Phe Arg Tyr Phe Tyr Asn Arg Thr Ser Lys		
25	30	35
Arg Cys Glu Thr Phe Val Phe Ser Gly Cys Asn Gly Asn Leu Asn Asn		
45	50	55
Phe Lys Leu Lys Ile Glu Arg Glu Val Ala Cys Val Ala Lys Tyr Lys		
60	65	70
Pro Pro Arg		
75		

<210> 178  
<211> 95  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -37..-1

<400> 178  
Met Ala Ser Pro Ala Val Asn Arg Trp Lys Arg Pro Arg Leu Lys Pro  
-35 -30 -25  
Val Trp Pro Arg Arg Leu Glu Ser Trp Leu Leu Asp Ala Leu Leu  
-20 -15 -10  
Arg Leu Gly Asp Thr Lys Lys Arg Gln Pro Glu Ala Ala Thr Lys  
-5 1 5 10  
Ser Cys Val Arg Ser Ser Cys Gly Gly Pro Ser Gly Asp Gly Pro Pro  
15 20 25  
Pro Cys Leu Gln Gln Pro Asp Pro Arg Ala Leu Ser Gln Ala Phe Ser  
30 35 40  
Arg Ser Phe Pro Leu Phe Pro Ser Leu Ala Gly Lys Ser Met Ile  
45 50 55

<210> 179  
<211> 121  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -23..-1

<400> 179  
Met Met Leu Pro Gln Trp Leu Leu Leu Phe Leu Leu Phe Phe Phe  
-20 -15 -10  
Leu Phe Leu Leu Thr Arg Gly Ser Leu Ser Pro Thr Lys Tyr Asn Leu  
-5 1 5  
Leu Glu Leu Lys Glu Ser Cys Ile Arg Asn Gln Asp Cys Glu Thr Gly  
10 15 20 25  
Cys Cys Gln Arg Ala Pro Asp Asn Cys Glu Ser His Cys Ala Glu Lys  
30 35 40  
Gly Ser Glu Gly Ser Leu Cys Gln Thr Gln Val Phe Phe Gly Gln Tyr  
45 50 55  
Arg Ala Cys Pro Cys Leu Arg Asn Leu Thr Cys Ile Tyr Ser Lys Asn  
60 65 70  
Glu Lys Trp Leu Ser Ile Ala Tyr Gly Arg Cys Gln Lys Ile Gly Arg  
75 80 85  
Gln Lys Leu Ala Lys Lys Met Phe Phe  
90 95

<210> 180  
<211> 59  
<212> PRT  
<213> Homo sapiens

<400> 180  
Met Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg

1	5	10	15												
Gln	Ile	Gln	Val	Leu	Lys	Met	Leu	Pro	Arg	Glu	Lys	Leu	Arg	Arg	Arg
			20				25					30			
Glu	Glu	Arg	Lys	Gln	Ile	Asn	Gly	Lys	Lys	Glu	Arg	Thr	Lys	Tyr	Glu
			35				40					45			
Thr	Pro	Arg	Lys	Arg	Glu	Gly	Lys	Lys	Lys	Lys					
			50				55								

<210> 181  
<211> 86  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -14..-1

<400> 181  
Met Val Ala Leu Asn Leu Ile Leu Val Pro Cys Cys Ala Ala Trp Cys  
-10 -5 1  
Asp Pro Arg Arg Ile His Ser Gln Asp Asp Val Pro Arg Ser Ser Ala  
5 10 15  
Ala Asp Thr Gly Ser Ala Met Gln Arg Arg Glu Ala Trp Ala Gly Trp  
20 25 30  
Arg Arg Ser Gln Pro Phe Ser Val Gly Leu Pro Ser Ala Glu Arg Leu  
35 40 45 50  
Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg Ser Leu Val Gly Glu Gly  
55 60 65  
Tyr Arg Ile Cys Asp Leu  
70

<210> 182  
<211> 165  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -58..-1

<400> 182  
Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro Ile  
-55 -50 -45  
Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser Pro  
-40 -35 -30  
Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu Leu  
-25 -20 -15  
Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala Val  
-10 -5 1 5  
Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Val Ser Phe Leu  
10 15 20  
Thr Phe Asp Leu Leu His Arg Pro Ala Gly His Thr Leu Pro Gln Arg  
25 30 35  
Lys Leu Leu Thr Arg Gly Gln Ser Gln Gly Ala Gly Glu Gly Pro Gly  
40 45 50  
Gln Gln Glu Ala Leu Leu Leu Gln Met Gly Thr Val Ser Gly Gln Leu  
55 60 65 70  
Ser Leu Gln Asp Ala Leu Leu Leu Leu Met Gly Leu Gly Pro Leu

	75	80	85
Leu Arg Ala Cys Gly Met Pro Leu Thr	Leu	Leu	Gly Leu Ala Phe Cys
90	95		100
Leu His Pro Trp Ala			
	105		

<210> 183  
<211> 80  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -35..-1

<400> 183  
Met Pro Phe Gln Phe Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly  
-35           -30           -25           -20  
Gly Asp Ser Ser Ile Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala  
              -15           -10           -5  
Cys Asn Gly Lys Glu Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro  
              1            5            10  
Gly Ser His Cys Leu Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala  
              15           20           25  
Thr Thr Arg Lys Pro Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys  
30           35           40           45

<210> 184  
<211> 73  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -21..-1

<400> 184  
Met Ala Pro Gln Thr Leu Leu Pro Val Leu Val Leu Cys Val Leu Leu  
-20           -15           -10  
Leu Gln Ala Gln Gly Gly Tyr Arg Asp Lys Met Arg Met Gln Arg Ile  
-5            1            5           10  
Lys Val Cys Glu Lys Arg Pro Ser Ile Asp Leu Cys Ile His His Cys  
              15           20           25  
Ser Cys Phe Gln Lys Cys Glu Thr Asn Lys Ile Cys Cys Ser Ala Phe  
              30           35           40  
Cys Gly Asn Ile Cys Met Ser Ile Leu  
        45           50

<210> 185  
<211> 98  
<212> PRT  
<213> Homo sapiens

<400> 185  
Met Leu Gly Ala Glu Thr Glu Glu Lys Leu Phe Asp Ala Pro Leu Ser  
1           5           10           15

Ile Ser Lys Arg Glu Gln Leu Glu Gln Gln Val Pro Glu Asn Tyr Phe  
 20 25 30  
 Tyr Val Pro Asp Leu Gly Gln Val Pro Glu Ile Asp Val Pro Ser Tyr  
 35 40 45  
 Leu Pro Asp Leu Pro Gly Ile Ala Asn Asp Leu Met Tyr Ile Ala Asp  
 50 55 60  
 Leu Gly Pro Gly Ile Ala Pro Ser Ala Pro Gly Thr Ile Pro Glu Leu  
 65 70 75 80  
 Pro Thr Phe His Thr Glu Val Ala Glu Pro Leu Lys Thr Tyr Lys Met  
 85 90 95  
 Gly Tyr

<210> 186  
<211> 112  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -21...-1

<400> 186  
Met Glu Ser Arg Val Leu Leu Arg Thr Phe Cys Leu Ile Phe Gly Leu  
-20 -15 -10  
Gly Ala Val Trp Gly Leu Gly Val Asp Pro Ser Leu Gln Ile Asp Val  
-5 1 5 10  
Leu Thr Glu Leu Glu Leu Gly Glu Ser Thr Thr Gly Val Arg Gln Val  
15 20 25  
Pro Gly Leu His Asn Gly Thr Lys Ala Phe Leu Phe Gln Asp Thr Pro  
30 35 40  
Arg Ser Ile Lys Ala Ser Thr Ala Thr Ala Glu Gln Phe Phe Gln Lys  
45 50 55  
Leu Arg Asn Lys His Glu Phe Thr Ile Leu Val Thr Leu Lys Gln Thr  
60 65 70 75  
His Leu Asn Ser Gly Val Ile Leu Ser Ile His His Leu Asp His Arg  
80 85 90

<210> 187  
<211> 70  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -44...-1

<400> 187  
Met Cys Cys Tyr Cys Arg Ile Phe Cys Leu Arg Cys Thr Tyr Phe Pro  
-40 -35 -30  
Val His Cys Gly Met Cys Asn Leu Arg Tyr Phe Glu Phe Ser Thr Phe  
-25 -20 -15  
Leu Leu Ser Leu Ser Leu Ile Thr Tyr Cys Phe Trp Asp Pro Pro His  
-10 -5 1  
Arg Gly Ser His Ser Leu Ser Leu Glu His Thr Pro Leu Asp Phe Leu  
5 10 15 20  
Glu Trp Gly Leu Leu Arg  
25

<210> 188  
<211> 92  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -13...-1

<400> 188  
Met Leu Phe Ser Leu Ser Leu Leu Ser Asn Leu Asn Gln Ile Gly Ser  
-10 -5 1  
Ser His Leu Asp Arg Pro His Ile Pro Gly Gln Ser Ala Gln Leu Phe  
5 10 15  
Ile Tyr Gln Met Ser Ser Gln Gln Leu Gln Gln Pro Ser Ala Asn  
20 25 30 35  
Lys Lys Ala Gly Lys Ile His Asn Thr Pro Phe Ala Asn Gln Leu Asn  
40 45 50  
Pro Thr Gln His Leu Ala Lys Pro Phe Gln Gln Ile Leu Pro Gly Arg  
55 60 65  
Gln Ser Gly Ser Leu Thr Ser Pro Phe Leu Ala Cys  
70 75

<210> 189  
<211> 207  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -42...-1

<400> 189  
Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala  
-40 -35 -30  
Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe  
-25 -20 -15  
Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Pro Ile Ile  
-10 -5 1 5  
Leu Gln Glu Gln Lys Thr Val Leu Ala Ser Val Phe Ser Val Leu Ser  
10 15 20  
Ala Ile Tyr Ala Ser Gln Thr Glu Gln Glu Tyr Leu Lys Ile Glu Lys  
25 30 35  
Val Asp Leu Pro Leu Ile Asp Ser Leu Ile Arg Val Leu Gln Asn Met  
40 45 50  
Glu Gln Cys Gln Lys Lys Pro Glu Asn Ser Ala Glu Ser Asn Thr Glu  
55 60 65 70  
Glu Thr Lys Arg Thr Asp Leu Thr Gln Asp Asp Leu His Leu Lys Ile  
75 80 85  
Leu Lys Asp Ile Leu Cys Glu Phe Leu Ser Asn Ile Phe Gln Ala Leu  
90 95 100  
Thr Lys Glu Thr Val Ala Gln Gly Val Lys Glu Gly Gln Leu Ser Lys  
105 110 115  
Gln Lys Cys Ser Ser Ala Phe Gln Asn Leu Leu Pro Phe Tyr Ser Pro  
120 125 130  
Val Val Glu Asp Phe Ile Lys Ile Leu Arg Glu Val Asp Lys Ala Leu  
135 140 145 150  
Ala Asp Asp Leu Glu Lys Asn Phe Pro Ser Leu Lys Val Gln Thr

155

160

165

<210> 190  
 <211> 201  
 <212> PRT  
 <213> Homo sapiens

<400> 190  
 Met Gln Val Ala Leu Lys Glu Asp Leu Asp Ala Leu Lys Glu Lys Phe  
 1 5 10 15  
 Arg Thr Met Glu Ser Asn Gln Lys Ser Ser Phe Gln Glu Ile Pro Lys  
 20 25 30  
 Leu Asn Glu Glu Leu Leu Ser Lys Gln Lys Gln Leu Glu Lys Ile Glu  
 35 40 45  
 Ser Gly Glu Met Gly Leu Asn Lys Val Trp Ile Asn Ile Thr Glu Met  
 50 55 60  
 Asn Lys Gln Ile Ser Leu Leu Thr Ser Ala Val Asn His Leu Lys Ala  
 65 70 75 80  
 Asn Val Lys Ser Ala Ala Asp Leu Ile Ser Leu Pro Thr Thr Val Glu  
 85 90 95  
 Gly Leu Gln Lys Ser Val Ala Ser Ile Gly Asn Thr Leu Asn Ser Val  
 100 105 110  
 His Leu Ala Val Glu Ala Leu Gln Lys Thr Val Asp Glu His Lys Lys  
 115 120 125  
 Thr Met Glu Leu Leu Gln Ser Asp Met Asn Gln His Phe Leu Lys Glu  
 130 135 140  
 Thr Pro Gly Ser Asn Gln Ile Ile Pro Ser Pro Ser Ala Thr Ser Glu  
 145 150 155 160  
 Leu Asp Asn Lys Thr His Ser Glu Asn Leu Lys Gln Met Gly Asp Arg  
 165 170 175  
 Ser Ala Thr Leu Lys Arg Gln Ser Leu Asp Gln Val Thr Asn Arg Thr  
 180 185 190  
 Asp Thr Val Lys Ile Gln Lys Lys Lys  
 195 200

<210> 191  
 <211> 379  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -37...-1

<400> 191  
 Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His  
 -35 -30 -25  
 Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr  
 -20 -15 -10  
 Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val  
 -5 1 5 10  
 Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys  
 15 20 25  
 Ser Leu Ala Glu Glu Leu Arg His Ile His Ser Arg Tyr Arg Gly Ser  
 30 35 40  
 Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly  
 45 50 55  
 Ala Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala

60	65	70	75
Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln			
80	85		90
Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile			
95	100		105
Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala			
110	115		120
Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln			
125	130		135
Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly			
140	145		150
Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val			
160	165		170
Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys			
175	180		185
Leu Pro Gln Gln Thr Gly Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr			
190	195		200
Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Ala Gly Thr			
205	210		215
Cys Val Leu Glu Tyr Ala Thr Pro Leu Gln Thr Leu Phe Ala Met Ser			
220	225		230
Gln Tyr Ser Gln Ala Gly Phe Ser Arg Glu Asp Arg Leu Glu Gln Ala			
240	245		250
Lys Leu Phe Cys Arg Thr Leu Glu Asp Ile Leu Ala Asp Ala Pro Glu			
255	260		265
Ser Gln Asn Asn Cys Arg Leu Ile Ala Tyr Gln Glu Pro Ala Asp Asp			
270	275		280
Ser Ser Phe Ser Leu Ser Gln Glu Val Leu Arg His Leu Arg Gln Glu			
285	290		295
Glu Lys Glu Glu Val Thr Val Gly Ser Leu Lys Thr Ser Ala Val Pro			
300	305		310
Ser Thr Ser Thr Met Ser Gln Glu Pro Glu Leu Leu Ser Gly Met			
320	325		330
Gly Lys Pro Leu Pro Leu Arg Thr Asp Phe Ser			
335	340		

<210> 192  
<211> 112  
<212> PRT  
<213> *Homo sapiens*

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<400> 192
Met Pro Ser Glu Gly Arg Cys Trp Glu Thr Leu Lys Ala Leu Arg Ser
      5           10          15
1
Ser Asp Lys Gly Arg Leu Cys Tyr Tyr Arg Asp Trp Leu Leu Arg Arg
      20          25          30
Glu Asp Val Leu Glu Glu Cys Met Ser Leu Pro Lys Leu Ser Ser Tyr
      35          40          45
Ser Gly Trp Val Val Glu His Val Leu Pro His Met Gln Glu Asn Gln
      50          55          60
Pro Leu Ser Glu Thr Ser Pro Ser Ser Thr Ser Ala Ser Ala Leu Asp
65
      70          75          80
Gln Pro Ser Phe Val Pro Lys Ser Pro Asp Ala Ser Ser Ala Phe Ser
      85          90          95
Pro Ala Ser Pro Ala Thr Pro Asn Gly Thr Lys Gly Lys Lys Lys Lys
      100         105         110

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2103 193

<211> 43  
<212> PRT  
<213> Homo sapiens

<400> 193  
Ser Leu Pro Gln Ala Leu Trp Phe Gln Phe Phe Tyr His Ser Gly Ser  
1 5 10 15  
Ser Leu Glu Ser Pro Gly Met Leu Asn Gly Pro Phe Gln His Arg Asn  
20 25 30  
Ser Arg Ile Met Thr His Arg Ser Ala Glu Lys  
35 40

<210> 194  
<211> 51  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -16...-1

<400> 194  
Met Leu Arg Ile Ala Leu Thr Leu Ile Pro Ser Met Leu Ser Arg Ala  
-15 -10 -5  
Ala Gly Trp Cys Trp Tyr Lys Glu Pro Thr Gln Gln Phe Ser Tyr Leu  
1 5 10 15  
Cys Leu Pro Cys Leu Ser Trp Asn Lys Lys Gly Asn Val Leu Gln Leu  
20 25 30  
Pro Asn Phe  
35

<210> 195  
<211> 244  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -18...-1

<400> 195  
Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu Ala  
-15 -10 -5  
Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala Ser  
1 5 10  
Lys Glu Leu Gln Gln Ala Gln Thr Thr Arg Pro Glu Ser Thr Gln Ile  
15 20 25 30  
Gln Pro Gln Pro Gly Phe Cys Ile Lys Thr Asn Ser Ser Glu Gly Lys  
35 40 45  
Val Phe Ile Asn Ile Cys His Ser Pro Ser Ile Pro Pro Pro Ala Asp  
50 55 60  
Val Thr Glu Glu Glu Leu Leu Gln Met Leu Glu Glu Asp Gln Ala Gly  
65 70 75  
Phe Arg Ile Pro Met Ser Leu Gly Glu Pro His Ala Glu Leu Asp Ala  
80 85 90  
Lys Gly Gln Gly Cys Thr Ala Tyr Asp Val Ala Val Asn Ser Asp Phe  
95 100 105 110  
Tyr Arg Arg Met Gln Asn Ser Asp Phe Leu Arg Glu Leu Val Ile Thr

	115	120	125
Ile Ala Arg Glu Gly Leu Glu Asp Ile Tyr Asn Leu Gln Leu Asn Pro			
130	135	140	
Glu Trp Arg Met Met Lys Asn Arg Pro Phe Met Gly Ser Ile Ser Gln			
145	150	155	
Gln Asn Ile Arg Ser Glu Gln Arg Pro Arg Ile Gln Glu Leu Gly Asp			
160	165	170	
Leu Tyr Thr Pro Ala Pro Gly Arg Ala Glu Ser Gly Pro Glu Lys Pro			
175	180	185	190
His Leu Asn Leu Trp Leu Glu Ala Pro Asp Leu Leu Leu Ala Glu Val			
195	200	205	
Asp Leu Pro Lys Leu Asp Gly Ala Leu Gly Leu Ser Leu Glu Ile Gly			
210	215	220	
Arg Thr Ala Trp			
225			

<210> 196  
<211> 353  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -34..-1

	<400> 196	
Met Glu Arg Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly Tyr		
-30	-25	-20
Thr Gly Trp Ala Gly Ile Ala Val Leu Tyr Leu His Leu Tyr Asp Val		
-15	-10	-5
Phe Gly Asp Pro Ala Tyr Leu Gln Leu Ala His Gly Tyr Val Lys Gln		
1	5	10
Ser Leu Asn Cys Leu Thr Lys Arg Ser Ile Thr Phe Leu Cys Gly Asp		
15	20	25
Ala Gly Pro Leu Ala Val Ala Ala Val Leu Tyr His Lys Met Asn Asn		
35	40	45
Glu Lys Gln Ala Glu Asp Cys Ile Thr Arg Leu Ile His Leu Asn Lys		
50	55	60
Ile Asp Pro His Ala Pro Asn Glu Met Leu Tyr Gly Arg Ile Gly Tyr		
65	70	75
Ile Tyr Ala Leu Leu Phe Val Asn Lys Asn Phe Gly Val Glu Lys Thr		
80	85	90
Pro Gln Ser His Ile Gln Gln Ile Cys Glu Thr Ile Leu Thr Ser Gly		
95	100	105
Glu Asn Leu Ala Arg Lys Arg Asn Phe Thr Ala Lys Ser Pro Leu Met		
115	120	125
Tyr Glu Trp Tyr Gln Glu Tyr Tyr Val Gly Ala Ala His Gly Leu Ala		
130	135	140
Gly Ile Tyr Tyr Tyr Leu Met Gln Pro Ser Leu Gln Val Ser Gln Gly		
145	150	155
Lys Leu His Ser Leu Val Lys Pro Ser Val Asp Tyr Val Cys Gln Leu		
160	165	170
Lys Phe Pro Ser Gly Asn Tyr Pro Pro Cys Ile Gly Asp Asn Arg Asp		
175	180	185
Leu Leu Val His Trp Cys His Gly Ala Pro Gly Val Ile Tyr Met Leu		
195	200	205
Ile Gln Ala Tyr Lys Val Phe Arg Glu Glu Lys Tyr Leu Cys Asp Ala		
210	215	220
Tyr Gln Cys Ala Asp Val Ile Trp Gln Tyr Gly Leu Leu Lys Lys Gly		
225	230	235

Tyr Gly Leu Cys His Gly Ser Ala Gly Asn Ala Tyr Ala Phe Leu Thr  
 240 245 250  
 Leu Tyr Asn Leu Thr Gln Asp Met Lys Tyr Leu Tyr Arg Ala Cys Lys  
 255 260 265 270  
 Phe Ala Glu Trp Cys Leu Glu Tyr Gly Glu His Gly Cys Arg Thr Pro  
 275 280 285  
 Asp Thr Pro Phe Ser Leu Phe Glu Gly Met Ala Gly Thr Ile Tyr Phe  
 290 295 300  
 Leu Ala Asp Leu Leu Val Pro Thr Lys Ala Arg Phe Pro Ala Phe Glu  
 305 310 315  
 Leu

<210> 197  
<211> 30  
<212> PRT  
<213> Homo sapiens

<400> 197  
Met Gln Met Asp Thr Phe Phe Met Ser Glu Lys His Thr His Thr His  
1 5 10 15  
Thr His Ile His Thr His Thr Arg Lys Thr Lys Lys Lys Lys  
20 25 30

<210> 198  
<211> 112  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -48...-1

<400> 198  
Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly Phe Gly  
-45 -40 -35  
Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val Lys Ala  
-30 -25 -20  
Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser Leu Ala  
-15 -10 -5  
Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val Trp Val  
1 5 10 15  
Phe Leu Ala Thr Ser Gly Thr Leu Ala Gly Ile Met Gly Met Arg Phe  
20 25 30  
Tyr His Ser Gly Lys Phe Met Pro Ala Gly Leu Ile Ala Gly Ala Ser  
35 40 45  
Leu Leu Met Val Ala Lys Val Gly Val Ser Met Phe Asn Arg Pro His  
50 55 60

<210> 199  
<211> 54  
<212> PRT  
<213> Homo sapiens

<400> 199  
Glu Ile Ala Gly Tyr Gly Ala Glu Gly Phe Ser Ser Val Leu Gly Tyr  
1 5 10 15

Pro Arg Trp His Arg Leu Pro Pro Gln Ser Leu Gln His His Gln Tyr  
   20                         25                         30  
 Cys Gln Arg Arg Trp Pro Asp Arg Arg Cys Leu Gln Ser His Thr Gln  
   35                         40                         45  
 Ser Ser Gly His Leu Pro  
   50

<210> 200  
<211> 151  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -21...-1

<400> 200  
Met Ala Ala Ser Thr Ser Met Xaa Pro Val Ala Val Thr Ala Ala Val  
   -20                         -15                         -10  
Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu Arg Glu Ile  
   -5                         1                                 5                         10  
Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu Arg Gly Leu  
   15                         20                                 25  
Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser Leu Pro Ala  
   30                         35                                 40  
Leu Pro Xaa Gly Gln Leu Gln Pro Pro Pro Pro Ile Thr Glu Glu Asp  
   45                         50                                 55  
Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val  
   60                         65                                 70                         75  
Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys Asn Ser Lys  
   80                         85                                 90  
Lys Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Val Arg Ala Ile  
   95                         100                                 105  
Leu Lys Cys His Ser Ala Phe Ser Glu Thr Ser Ile Phe Arg Thr Asn  
   110                         115                                 120  
Gly Lys Val Lys Ser Phe Lys  
   125                         130

<210> 201  
<211> 228  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -25...-1

<400> 201  
Met Ser Met Ala Val Glu Thr Phe Gly Phe Phe Met Ala Thr Val Gly  
   -25                         -20                         -15                         -10  
Leu Leu Met Leu Gly Val Thr Leu Pro Asn Ser Tyr Trp Arg Val Ser  
   -5                         1                                 5  
Thr Val His Gly Asn Val Ile Thr Thr Asn Thr Ile Phe Glu Asn Leu  
   10                         15                                 20  
Trp Phe Ser Cys Ala Thr Asp Ser Leu Gly Val Tyr Asn Cys Trp Glu  
   25                         30                                 35  
Phe Pro Ser Met Leu Ala Leu Ser Gly Tyr Ile Gln Ala Cys Arg Ala  
   40                         45                                 50                         55

Leu Met Ile Thr Ala Ile Leu Leu Gly Phe Leu Gly Leu Leu Leu Gly  
           60                 65                 70  
 Ile Ala Gly Leu Arg Cys Thr Asn Ile Gly Gly Leu Glu Leu Ser Arg  
           75                 80                 85  
 Lys Ala Lys Leu Ala Ala Thr Ala Gly Ala Pro His Ile Leu Ala Gly  
           90                 95                 100  
 Ile Cys Gly Met Val Ala Ile Ser Trp Tyr Ala Phe Asn Ile Thr Arg  
           105                110                115  
 Asp Phe Asp Pro Leu Tyr Pro Gly Thr Lys Tyr Glu Leu Gly Pro  
           120                125                130                135  
 Ala Leu Tyr Leu Gly Trp Ser Ala Ser Leu Ile Ser Ile Leu Gly Gly  
           140                145                150  
 Leu Cys Leu Cys Ser Ala Cys Cys Gly Ser Asp Glu Asp Pro Ala  
           155                160                165  
 Ala Ser Ala Arg Arg Pro Tyr Gln Ala Pro Val Ser Val Met Pro Val  
           170                175                180  
 Ala Thr Ser Asp Gln Glu Gly Asp Ser Ser Phe Gly Lys Tyr Gly Arg  
           185                190                195  
 Asn Ala Tyr Val  
   200

<210> 202  
 <211> 64  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -47...-1

<400> 202  
 Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly  
       -45                -40                -35  
 Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser  
       -30                -25                -20  
 Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe  
       -15                -10                -5                1  
 Pro Asp Leu Pro Thr Glu Met Pro Leu Arg Ala Lys Gly Val Asn Thr  
       5                  10                 15

<210> 203  
 <211> 146  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -31...-1

<400> 203  
 Met Met Trp Gln Lys Tyr Ala Gly Ser Arg Arg Ser Met Pro Leu Gly  
       -30                -25                -20  
 Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala Gly Gly Phe Ala Ile  
       -15                -10                -5                1  
 Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg Ala Leu Tyr Tyr Lys  
       5                  10                 15  
 Leu Ala Val Glu Gln Leu Gln Ser His Pro Glu Ala Gln Glu Ala Leu  
       20                 25                 30

Gly Pro Pro Leu Asn Ile His Tyr Leu Lys Leu Ile Asp Arg Glu Asn  
   35               40               45  
 Phe Val Asp Ile Val Asp Ala Lys Leu Lys Ile Pro Val Ser Gly Ser  
   50               55               60               65  
 Lys Ser Glu Gly Leu Leu Tyr Val His Ser Ser Arg Gly Gly Pro Phe  
     70              75              80  
 Gln Arg Trp His Leu Asp Glu Val Phe Leu Glu Leu Lys Asp Gly Gln  
     85              90              95  
 Gln Ile Pro Val Phe Lys Leu Ser Gly Glu Asn Gly Asp Glu Val Lys  
   100             105             110  
 Lys Glu  
   115

<210> 204  
<211> 87  
<212> PRT  
<213> Homo sapiens

<400> 204  
Met Glu Leu Ala Pro Thr Ala Arg Leu Pro Pro Gly His Gly Ser Leu  
 1               5               10               15  
 Pro His Gly Val Leu Gly Pro Arg Ala Thr Gly Ser Val Thr His Leu  
   20              25              30  
 Ser Leu Leu Pro Gln Ile Lys Gln Arg Ala Ser Glu Ala Leu Pro Glu  
   35              40              45  
 Leu Leu Arg Pro Val Thr Pro Ile Thr Asn Phe Glu Gly Ser Gln Ser  
   50              55              60  
 Gln Asp His Ser Gly Ile Phe Gly Leu Val Thr Asn Leu Glu Glu Leu  
   65              70              75              80  
 Glu Val Asp Asp Trp Glu Phe  
   85

<210> 205  
<211> 40  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -27..-1  
  
<400> 205  
Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr  
   -25              -20              -15  
 Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly  
   -10              -5              1              5  
 Leu Ser Leu Arg Ser Ala Met Ser  
   10

<210> 206  
<211> 154  
<212> PRT  
<213> Homo sapiens

<400> 206  
Met Gly Ser Leu Ser Gly Leu Arg Leu Ala Ala Gly Ser Cys Phe Arg

1	5	10	15
Leu Cys Glu Arg Asp Val Ser Ser	Ser Leu Arg Leu Thr	Arg Ser Ser	
20	25	30	
Asp Leu Lys Arg Ile Asn Gly Phe Cys Thr Lys Pro Gln Glu Ser Pro			
35	40	45	
Gly Ala Pro Ser Arg Thr Tyr Asn Arg Val Pro Leu His Lys Pro Thr			
50	55	60	
Asp Trp Gln Lys Lys Ile Leu Ile Trp Ser Gly Arg Phe Lys Lys Glu			
65	70	75	80
Asp Glu Ile Pro Glu Thr Val Ser Leu Glu Met Leu Asp Ala Ala Lys			
85	90	95	
Asn Lys Met Arg Val Lys Ser Ser Tyr Leu Met Ile Ala Leu Thr Val			
100	105	110	
Val Gly Cys Ile Phe Met Val Ile Glu Gly Lys Lys Ala Ala Gln Arg			
115	120	125	
His Glu Thr Leu Thr Ser Leu Asn Leu Glu Lys Lys Ala Arg Leu Lys			
130	135	140	
Glu Glu Ala Ala Met Lys Ala Lys Thr Glu			
145	150		

<210> 207  
<211> 101  
<212> PRT  
<213> *Homo sapiens*

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<400> 207
Met Val Cys Glu Lys Cys Glu Lys Lys Leu Gly Thr Val Ile Thr Pro
      5          10          15
1
Asp Thr Trp Lys Asp Gly Ala Arg Asn Thr Thr Glu Ser Gly Gly Arg
      20          25          30
Lys Leu Asn Lys Asn Lys Ala Leu Thr Ser Lys Lys Ala Arg Phe Asp
      35          40          45
Pro Tyr Gly Lys Asn Lys Phe Ser Thr Cys Arg Ile Cys Lys Ser Ser
      50          55          60
Val His Gln Pro Gly Ser His Tyr Cys Gln Gly Cys Ala Tyr Lys Lys
      65          70          75          80
Gly Ile Cys Ala Met Cys Gly Lys Lys Val Leu Asp Thr Lys Asn Tyr
      85          90          95
Lys Gln Thr Ser Val
      100

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<210> 208  
<211> 456  
<212> PRT  
<213> *Homo sapiens*

<220>  
<221> SIGNAL  
<222> -22..-1

<400> 208  
 Met Phe Glu Glu Pro Glu Trp Ala Glu Ala Ala Pro Val Ala Ala Gly  
           -20                 -15                 -10  
 Leu Gly Pro Val Ile Ser Arg Pro Pro Pro Ala Ala Ser Ser Gln Asn  
       -5                  1                  5                  10  
 Lys Gly Ser Lys Arg Arg Gln Leu Leu Ala Thr Leu Arg Ala Leu Glu  
       15                  20                  25  
 Ala Ala Ser Leu Ser Gln His Pro Pro Ser Leu Cys Ile Ser Asp Ser

<210> 209  
<211> 98  
<212> PRT  
<213> *Homo sapiens*

<220>  
<221> SIGNAL  
<222> -17...-1

&lt;400&gt; 209

Met Pro Ser Ser Phe Phe Leu Leu Leu Gln Phe Phe Leu Arg Ile Asp  
-15 -10 -5  
Gly Val Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp  
1 5 10 15  
Lys Thr Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser  
20 25 30  
Ser Leu Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile  
35 40 45  
Ser Gln Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe  
50 55 60  
Pro Glu Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln  
65 70 75  
Val Glu  
80

&lt;210&gt; 210

&lt;211&gt; 83

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -29...-1

&lt;400&gt; 210

Met Thr Leu Leu Ser Phe Ala Ala Phe Thr Ala Ala Phe Ser Val Leu  
-25 -20 -15  
Pro Cys Tyr Tyr Leu Gly Leu Phe Gln Arg Ala Leu Ala Ser Val Phe  
-10 -5 1  
Asp Pro Leu Cys Val Cys Ser Arg Val Leu Pro Thr Pro Val Cys Thr  
5 10 15  
Leu Val Ala Thr Gln Ala Glu Lys Ile Leu Glu Asn Gly Pro Cys Pro  
20 25 30 35  
Thr Lys Glu Ala Ala Gln Leu Val Gly Lys Gly Ser Val Ser Ala Arg  
40 45 50  
Asn Ala Ser

&lt;210&gt; 211

&lt;211&gt; 229

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; -23...-1

&lt;400&gt; 211

Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Ala Ala  
-20 -15 -10  
Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu  
-5 1 5  
Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe  
10 15 20 25  
Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val  
30 35 40  
Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu

	45	50	55
Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr			
	60	65	70
Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe			
	75	80	85
Ser Thr Ile Ser Glu Lys Val Ile Phe Glu Leu Ile Leu Asp Asn			
	90	95	100
Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr			105
	110	115	120
Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile			
	125	130	135
Ser Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu			
	140	145	150
Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe			
	155	160	165
Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val			
	170	175	180
Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys			185
	190	195	200
Arg Lys Ser Arg Thr			
	205		

<210> 212  
<211> 152  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -21..-1

	400	212		
Met Ala Gln Leu Gly Ala Val Val Ala Val Ala Ser Ser Phe Phe Cys				
	-20	-15	-10	
Ala Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly His Ile Gly				
	-5	1	5	10
Val Tyr Tyr Arg Gly Gly Ala Leu Leu Thr Ser Thr Ser Gly Pro Gly				
	15	20	25	
Phe His Leu Met Leu Pro Phe Ile Thr Ser Tyr Lys Ser Val Gln Thr				
	30	35	40	
Thr Leu Gln Thr Asp Glu Val Lys Asn Val Pro Cys Gly Thr Ser Gly				
	45	50	55	
Gly Val Met Ile Tyr Phe Asp Arg Ile Glu Val Val Asn Phe Leu Val				
	60	65	70	75
Pro Asn Ala Val His Asp Ile Val Lys Asn Tyr Thr Ala Asp Tyr Asp				
	80	85	90	
Lys Ala Leu Ile Phe Asn Lys Ile His His Glu Leu Asn Gln Phe Cys				
	95	100	105	
Ser Val His Thr Leu Gln Glu Val Tyr Ile Glu Leu Phe Gly Leu Glu				
	110	115	120	
Asn Asp Phe Ser Gln Glu Ser Ser				
	125	130		

<210> 213  
<211> 179  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -54..-1

&lt;400&gt; 213

Met	Ala	Ala	Ser	Glu	Ala	Ala	Val	Val	Ser	Ser	Pro	Ser	Leu	Lys	Thr
				-50					-45				-40		
Asp	Thr	Ser	Pro	Val	Leu	Glu	Thr	Ala	Gly	Thr	Val	Ala	Ala	Met	Ala
				-35					-30				-25		
Ala	Thr	Pro	Ser	Ala	Arg	Ala	Ala	Ala	Ala	Ala	Val	Val	Ala	Ala	Ala
				-20					-15				-10		
Arg	Thr	Gly	Ser	Glu	Ala	Arg	Val	Ser	Lys	Ala	Ala	Leu	Ala	Thr	Lys
				-5					1			5			10
Leu	Leu	Ser	Leu	Ser	Gly	Val	Phe	Ala	Val	His	Lys	Pro	Lys	Gly	Pro
				15					20				25		
Thr	Ser	Ala	Glu	Leu	Leu	Asn	Arg	Leu	Lys	Glu	Lys	Leu	Leu	Ala	Glu
				30					35				40		
Ala	Gly	Met	Pro	Ser	Pro	Glu	Trp	Thr	Lys	Arg	Lys	Lys	Gln	Thr	Leu
				45					50				55		
Lys	Ile	Gly	His	Gly	Gly	Thr	Leu	Asp	Ser	Ala	Ala	Arg	Gly	Val	Leu
				60					65				70		
Val	Val	Gly	Ile	Gly	Ser	Gly	Thr	Lys	Met	Leu	Thr	Ser	Met	Leu	Ser
				75					80			85			90
Gly	Ser	Lys	Arg	Tyr	Thr	Ala	Ile	Gly	Glu	Leu	Gly	Lys	Ala	Thr	Asp
				95					100				105		
Thr	Leu	Asp	Ser	Thr	Gly	Lys	Val	Thr	Glu	Glu	Lys	Pro	Tyr	Gly	Met
				110					115				120		
Asn	Leu	Ile													
		125													

<210> 214  
<211> 269  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -92..-1

&lt;400&gt; 214

Met	Ile	Thr	His	Val	Thr	Leu	Glu	Asp	Ala	Leu	Ser	Asn	Val	Asp	Leu
				-90					-85				-80		
Leu	Glu	Glu	Leu	Pro	Leu	Pro	Asp	Gln	Gln	Pro	Cys	Ile	Glu	Pro	Pro
				-75					-70				-65		
Pro	Ser	Ser	Ile	Met	Tyr	Gln	Ala	Asn	Phe	Asp	Thr	Asn	Phe	Glu	Asp
				-60					-55				-50		-45
Arg	Asn	Ala	Phe	Val	Thr	Gly	Ile	Ala	Arg	Tyr	Ile	Glu	Gln	Ala	Thr
				-40					-35				-30		
Val	His	Ser	Ser	Met	Asn	Glu	Met	Leu	Glu	Glu	Gly	His	Glu	Tyr	Ala
				-25					-20				-15		
Val	Met	Leu	Tyr	Thr	Trp	Arg	Ser	Cys	Ser	Arg	Ala	Ile	Pro	Gln	Val
				-10					-5				1		
Lys	Cys	Asn	Glu	Gln	Pro	Asn	Arg	Val	Glu	Ile	Tyr	Glu	Lys	Thr	Val
				5					10			15			20
Glu	Val	Leu	Glu	Pro	Glu	Val	Thr	Lys	Leu	Met	Lys	Phe	Met	Tyr	Phe
				25					30				35		
Gln	Arg	Lys	Ala	Ile	Glu	Arg	Phe	Cys	Ser	Glu	Val	Lys	Arg	Leu	Cys
				40					45				50		
His	Ala	Glu	Arg	Arg	Lys	Asp	Phe	Val	Ser	Glu	Ala	Tyr	Leu	Leu	Thr
				55					60				65		

Leu Gly Lys Phe Ile Asn Met Phe Ala Val Leu Asp Glu Leu Lys Asn  
 70 75 80  
 Met Lys Cys Ser Val Lys Asn Asp His Ser Ala Tyr Lys Arg Ala Ala  
 85 90 95 100  
 Gln Phe Leu Arg Lys Met Ala Asp Pro Gln Ser Ile Gln Glu Ser Gln  
 105 110 115  
 Asn Leu Ser Met Phe Leu Ala Asn His Asn Arg Ile Thr Gln Cys Leu  
 120 125 130  
 His Gln Gln Leu Glu Val Ile Pro Gly Tyr Glu Glu Leu Leu Ala Asp  
 135 140 145  
 Ile Val Asn Ile Cys Val Asp Tyr Tyr Glu Asn Lys Met Tyr Leu Thr  
 150 155 160  
 Pro Ser Glu Lys His Met Leu Leu Lys Val Lys Leu Pro  
 165 170 175

<210> 215  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -22...-1

<400> 215  
 Met Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu Trp Leu Ala Leu Val  
 -20 -15 -10  
 Asp Gly Leu Val Arg Ser Ser Pro Ser Leu Asp Gln Met Phe Asp Ala  
 -5 1 5 10  
 Glu Ile Leu Gly Phe Ser Thr Pro Pro Gly Arg Leu Ser Met Met Ser  
 15 20 25  
 Phe Ile Phe Asn Ala Leu Thr Cys Ala Leu Gly Leu Leu Tyr Phe Ile  
 30 35 40  
 Arg Arg Gly Lys Gln Cys Leu Asp Phe Thr Val Thr Val His Phe Phe  
 45 50 55  
 His Leu Leu Gly Cys Trp Phe Tyr Ser Ser Arg Phe Pro Ser Ala Leu  
 60 65 70  
 Thr Trp Trp Leu Val Gln Ala Val Cys Ile Ala Leu Met Ala Val Ile  
 75 80 85 90  
 Gly Glu Tyr Leu Cys Met Arg Thr Glu Leu Lys Glu Ile Pro Leu Asn  
 95 100 105  
 Ser Ala Pro Lys Ser Asn Val  
 110

<210> 216  
 <211> 67  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -38...-1

<400> 216  
 Met Asn Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser  
 -35 -30 -25  
 Val Lys Gly His Val Lys Met Leu Arg Leu Val Phe Ala Leu Val Thr  
 -20 -15 -10

Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu  
 -5 1 5 10  
 Phe Asn Pro Asn Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys  
 15 20 25  
 Glu Val Leu

<210> 217  
<211> 125  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -54...-1

<400> 217  
Met Ala Asp Glu Glu Leu Glu Ala Leu Arg Arg Gln Arg Leu Ala Glu  
-50 -45 -40  
Leu Gln Ala Lys His Gly Asp Pro Gly Asp Ala Ala Gln Gln Glu Ala  
-35 -30 -25  
Lys His Arg Glu Ala Glu Met Arg Asn Ser Ile Leu Ala Gln Val Leu  
-20 -15 -10  
Asp Gln Ser Ala Arg Ala Arg Leu Ser Asn Leu Ala Leu Val Lys Pro  
-5 1 5 10  
Glu Lys Thr Lys Ala Val Glu Asn Tyr Leu Ile Gln Met Ala Arg Tyr  
15 20 25  
Gly Gln Leu Ser Glu Lys Val Ser Glu Gln Gly Leu Ile Glu Ile Leu  
30 35 40  
Lys Lys Val Ser Gln Gln Thr Glu Lys Thr Thr Thr Val Lys Phe Asn  
45 50 55  
Arg Arg Lys Val Met Asp Ser Asp Glu Asp Asp Asp Tyr  
60 65 70

<210> 218  
<211> 376  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -21...-1

<400> 218  
Met Gly His Arg Phe Leu Arg Gly Leu Leu Thr Leu Leu Pro Pro  
-20 -15 -10  
Pro Pro Leu Tyr Thr Arg His Arg Met Leu Gly Pro Glu Ser Val Pro  
-5 1 5 10  
Pro Pro Lys Arg Ser Arg Ser Lys Leu Met Ala Pro Pro Arg Ile Gly  
15 20 25  
Thr His Asn Gly Thr Phe His Cys Asp Glu Ala Leu Ala Cys Ala Leu  
30 35 40  
Leu Arg Leu Leu Pro Glu Tyr Arg Asp Ala Glu Ile Val Arg Thr Arg  
45 50 55  
Asp Pro Glu Lys Leu Ala Ser Cys Asp Ile Val Val Asp Val Gly Gly  
60 65 70 75  
Glu Tyr Asp Pro Arg Arg His Arg Tyr Asp His His Gln Arg Ser Phe  
80 85 90  
Thr Glu Thr Met Ser Ser Leu Ser Pro Gly Arg Pro Trp Gln Thr Lys

	95	100	105
Leu Ser Ser Ala Gly Leu Ile Tyr	Leu His Phe Gly His	Lys Leu Leu	
110	115	120	
Ala Gln Leu Leu Gly Thr Ser Glu Glu Asp Ser Met Val Gly Thr Leu			
125	130	135	
Tyr Asp Lys Met Tyr Glu Asn Phe Val Glu Val Asp Ala Val Asp			
140	145	150	155
Asn Gly Ile Ser Gln Trp Ala Glu Gly Glu Pro Arg Tyr Ala Leu Thr			
160	165	170	
Thr Thr Leu Ser Ala Arg Val Ala Arg Leu Asn Pro Thr Trp Asn His			
175	180	185	
Pro Asp Gln Asp Thr Glu Ala Gly Phe Lys Arg Ala Met Asp Leu Val			
190	195	200	
Gln Glu Glu Phe Leu Gln Arg Leu Asp Phe Tyr Gln His Ser Trp Leu			
205	210	215	
Pro Ala Arg Ala Leu Val Glu Glu Ala Leu Ala Gln Arg Phe Gln Val			
220	225	230	235
Asp Pro Ser Gly Glu Ile Val Glu Leu Ala Lys Gly Ala Cys Pro Trp			
240	245	250	
Lys Glu His Leu Tyr His Leu Glu Ser Gly Leu Ser Pro Pro Val Ala			
255	260	265	
Ile Phe Phe Val Ile Tyr Thr Asp Gln Ala Gly Gln Trp Arg Ile Gln			
270	275	280	
Cys Val Pro Lys Glu Pro His Ser Phe Gln Ser Arg Leu Pro Leu Pro			
285	290	295	
Glu Pro Trp Arg Gly Leu Arg Asp Glu Ala Leu Asp Gln Val Ser Gly			
300	305	310	315
Ile Pro Gly Cys Ile Phe Val His Ala Ser Gly Phe Ile Gly Gly His			
320	325	330	
Arg Thr Arg Glu Gly Ala Leu Ser Met Ala Arg Ala Thr Leu Ala Gln			
335	340	345	
Arg Ser Tyr Leu Pro Gln Ile Ser			
350	355		

<210> 219  
<211> 211  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -30...1

<400> 219  
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val  
-30           -25           -20           -15  
Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro  
-10           -5           1  
Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu  
5           10           15  
Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu  
20           25           30  
Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly  
35           40           45           50  
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly  
55           60           65  
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Val Pro Arg Met  
70           75           80  
Glu Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe  
85           90           95

His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro  
 100 105 110  
 Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser  
 115 120 125 130  
 Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly  
 135 140 145  
 Thr His Lys Asp Val Leu Glu Gly Thr Glu Ser Ser Ser His Ser  
 150 155 160  
 Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser  
 165 170 175  
 Arg Gln Leu  
 180

<210> 220  
 <211> 154  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -60...-1

<400> 220  
 Met Gly Ser Lys Cys Cys Lys Gly Gly Pro Asp Glu Asp Ala Val Glu  
 -60 -55 -50 -45  
 Arg Gln Arg Arg Gln Lys Leu Leu Leu Ala Gln Leu His His Arg Lys  
 -40 -35 -30  
 Arg Val Lys Ala Ala Gly Gln Ile Gln Ala Trp Trp Arg Gly Val Leu  
 -25 -20 -15  
 Val Arg Arg Thr Leu Leu Val Ala Ala Leu Arg Ala Trp Met Ile Gln  
 -10 -5 1  
 Cys Trp Trp Arg Thr Leu Val Gln Arg Arg Ile Arg Gln Arg Arg Gln  
 5 10 15 20  
 Ala Leu Leu Arg Val Tyr Val Ile Gln Glu Gln Ala Thr Val Lys Leu  
 25 30 35  
 Gln Ser Cys Ile Arg Met Trp Gln Cys Arg Gln Cys Tyr Arg Gln Met  
 40 45 50  
 Cys Asn Ala Leu Cys Leu Phe Gln Val Pro Glu Ser Ser Leu Ala Phe  
 55 60 65  
 Gln Thr Asp Gly Phe Leu Gln Val Gln Tyr Ala Ile Pro Ser Lys Gln  
 70 75 80  
 Pro Glu Phe His Ile Glu Ile Leu Ser Ile  
 85 90

<210> 221  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -42...-1

<400> 221  
 Met Lys Gly Gly Ala Phe Ser Asn Leu Asn Asp Ser Gln Leu Ser Ala  
 -40 -35 -30  
 Ser Phe Leu Gln Pro Ser Leu Gln Ala Asn Cys Pro Ala Leu Asp Pro  
 -25 -20 -15

Ala Val Ser Leu Ser Ala Pro Ala Phe Ala Ser Ala Leu Arg Ser Met  
 -10 -5 1 5  
 Lys Ser Ser Gln Ala Ala Arg Lys Asp Asp Phe Leu Arg Ser Leu Ser  
 10 15 20  
 Asp Gly Asp Ser Gly Thr Ser Glu His Ile Ser Ala Val Val Thr Ser  
 25 30 35  
 Pro Arg Ile Ser Cys His Gly Ala Ala Ile Pro Thr Ala Arg Ala Leu  
 40 45 50  
 Cys Leu Gly Cys Ser Cys Cys Thr Glu Arg Leu Leu Leu Pro Pro Pro  
 55 60 65 70  
 Ser Leu Leu Ser Leu Glu Ala Pro Ala Ser Thr  
 75 80

<210> 222  
 <211> 346  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -19...-1

<400> 222  
 Met Ala Met Ala Gln Lys Leu Ser His Leu Leu Pro Ser Leu Arg Gln  
 -15 -10 -5  
 Val Ile Gln Glu Pro Gln Leu Ser Leu Gln Pro Glu Pro Val Phe Thr  
 1 5 10  
 Val Asp Arg Ala Glu Val Pro Pro Leu Phe Trp Lys Pro Tyr Ile Tyr  
 15 20 25  
 Ala Gly Tyr Arg Pro Leu His Gln Thr Trp Arg Phe Tyr Phe Arg Thr  
 30 35 40 45  
 Leu Phe Gln Gln His Asn Glu Ala Val Asn Val Trp Thr His Leu Leu  
 50 55 60  
 Ala Ala Leu Val Leu Leu Arg Leu Ala Leu Phe Val Glu Thr Val  
 65 70 75  
 Asp Phe Trp Gly Asp Pro His Ala Leu Pro Leu Phe Ile Ile Val Leu  
 80 85 90  
 Ala Ser Phe Thr Tyr Leu Ser Leu Ser Ala Leu Ala His Leu Leu Gln  
 95 100 105  
 Ala Lys Ser Glu Phe Trp His Tyr Ser Phe Phe Leu Asp Tyr Val  
 110 115 120 125  
 Gly Val Ala Val Tyr Gln Phe Gly Ser Ala Leu Ala His Phe Tyr Tyr  
 130 135 140  
 Ala Ile Glu Pro Ala Trp His Ala Gln Val Gln Ala Val Phe Leu Pro  
 145 150 155  
 Met Ala Ala Phe Leu Ala Trp Leu Ser Cys Ile Gly Ser Cys Tyr Asn  
 160 165 170  
 Lys Tyr Ile Gln Lys Pro Gly Leu Leu Gly Arg Thr Cys Gln Glu Val  
 175 180 185  
 Pro Ser Val Leu Ala Tyr Ala Leu Asp Ile Ser Pro Val Val His Arg  
 190 195 200 205  
 Ile Phe Val Ser Ser Asp Pro Thr Thr Asp Asp Pro Ala Leu Leu Tyr  
 210 215 220  
 His Lys Cys Gln Val Val Phe Phe Leu Leu Ala Ala Phe Phe Ser  
 225 230 235  
 Thr Phe Met Pro Glu Arg Trp Phe Pro Gly Ser Cys His Val Phe Gly  
 240 245 250  
 Gln Gly His Gln Leu Phe His Ile Phe Leu Val Leu Cys Thr Leu Ala  
 255 260 265  
 Gln Leu Glu Ala Val Ala Leu Asp Tyr Glu Ala Arg Arg Pro Ile Tyr

270	275	280	285
Glu Pro Leu His Thr His Trp Pro His Asn Phe Ser Gly Leu Phe Leu			
290	295	300	
Leu Thr Val Gly Ser Ser Ile Leu Thr Ala Phe Leu Leu Ser Gln Leu			
305	310	315	
Val Gln Arg Lys Leu Asp Gln Lys Thr Lys			
320	325		

<210> 223  
<211> 210  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -20..-1

<400> 223  
Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser  
-20           -15           -10           -5  
Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp  
1               5           10  
Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys  
15              20           25  
Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr  
30              35           40  
Asn Asp Ala Leu Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Arg Arg  
45              50           55           60  
Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg  
65              70           75  
Thr Glu Ser Phe Asp Val Val Thr Lys Cys Val Ser Phe Thr Leu Thr  
80              85           90  
Glu Gln Phe Met Glu Lys Phe Val Asp Pro Gly Asn His Asn Ser Gly  
95              100          105  
Ile Asp Leu Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu Leu Pro  
110             115          120  
Phe Val Ser Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys  
125             130          135          140  
Ala Cys Ile Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu  
145             150          155  
His Leu Leu Ala Val Thr Lys Glu Ser Met Leu Pro Ala Gly Ala Glu  
160             165          170  
Ser Lys His Thr Ala Thr Pro Ala His Ala Cys Val Gln Thr Gly Lys  
175             180          185  
Pro Lys  
190

<210> 224  
<211> 184  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -20..-1

<400> 224  
Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser

-20	-15	-10	-5
Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp			
1	5	10	
Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys			
15	20	25	
Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr			
30	35	40	
Asn Asp Ala Pro Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Arg Arg			
45	50	55	60
Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg			
65	70	75	
Thr Glu Ser Phe Asp Val Val Thr Lys Cys Val Ser Phe Thr Leu Thr			
80	85	90	
Glu Gln Phe Met Glu Lys Phe Val Asp Pro Gly Asn His Asn Ser Gly			
95	100	105	
Ile Asp Leu Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu Leu Pro			
110	115	120	
Phe Val Ser Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys			
125	130	135	140
Ala Cys Ile Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu			
145	150	155	
His Leu Leu Ala Asp Thr Met Leu			
160			

<210> 225  
<211> 227  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -22...-1

<400> 225			
Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Gly Leu			
-20	-15	-10	
Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His			
-5	1	5	10
Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val			
15	20	25	
Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys			
30	35	40	
Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys			
45	50	55	
Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp			
60	65	70	
Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His			
75	80	85	90
Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile			
95	100	105	
Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His			
110	115	120	
Ser Gly Phe His Arg Tyr Gln Phe Val Tyr Leu Gln Glu Gly Lys			
125	130	135	
Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys			
140	145	150	
Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser			
155	160	165	170
Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala			
175	180	185	

Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile  
190 195 200  
Ala Ala Cys  
205

<210> 226  
<211> 74  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -41...-1

<400> 226  
Met Ile Ala Arg Arg Asn Pro Val Pro Leu Arg Phe Leu Pro Asp Glu  
-40 -35 -30  
Ala Arg Ser Leu Pro Pro Pro Lys Leu Thr Asp Pro Arg Leu Leu Tyr  
-25 -20 -15 -10  
Ile Gly Phe Leu Gly Tyr Cys Ser Gly Leu Ile Asp Asn Leu Ile Arg  
-5 1 5  
Arg Arg Pro Ile Ala Thr Ala Gly Leu His Arg Gln Leu Leu Tyr Ile  
10 15 20  
Thr Ala Phe Phe Leu Leu Asp Ile Ile Leu  
25 30

<210> 227  
<211> 73  
<212> PRT  
<213> Homo sapiens

<400> 227  
Met Glu Lys Tyr Glu Asn Leu Gly Leu Val Gly Glu Gly Ser Tyr Gly  
1 5 10 15  
Met Val Met Lys Cys Arg Asn Lys Asp Thr Gly Arg Ile Val Ala Ile  
20 25 30  
Lys Lys Phe Leu Glu Ser Asp Asp Lys Met Val Lys Lys Ile Ala  
35 40 45  
Met Arg Glu Val Lys Leu Leu Lys Gln Leu Arg His Glu Asn Leu Val  
50 55 60  
Asn Leu Leu Glu Val Cys Lys Lys Lys  
65 70

<210> 228  
<211> 82  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -16...-1

<400> 228  
Met Lys Arg Leu Leu Pro Ala Thr Ser Leu Ala Gly Pro Val Leu Ser  
-15 -10 -5  
Thr Leu Ile Ala Pro Thr Pro Met Leu Phe Cys Glu Asp Lys Ser Trp

1 5 10 15  
Asp Leu Phe Leu Phe Phe Lys Ser His Lys Thr Trp Gly Ile Ser Thr  
20 25 30  
Asn Leu Ser Ser Cys Pro Phe Gly Asn Leu Phe Leu Cys Val Gln Phe  
35 40 45  
Val Arg Glu Lys Gln Ser Phe Cys Met Asn Thr Glu Cys Asp Leu Arg  
50 55 60  
Lys Asn  
65

<210> 229  
<211> 119  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -56..-1

<400> 229  
Met Ala Glu Pro Ser Ala Ala Thr Gln Ser His Ser Ile Ser Ser Ser  
-55 -50 -45  
Ser Phe Gly Ala Glu Pro Ser Ala Pro Gly Gly Gly Ser Pro Gly  
-40 -35 -30 -25  
Ala Cys Pro Ala Leu Gly Thr Lys Ser Cys Ser Ser Ser Cys Ala Asp  
-20 -15 -10  
Ser Phe Val Ser Ser Ser Ser Gln Pro Val Ser Leu Phe Ser Thr  
-5 1 5  
Ser Gln Glu Gly Leu Ser Ser Leu Cys Ser Asp Glu Pro Ser Ser Glu  
10 15 20  
Ile Met Thr Ser Ser Phe Leu Ser Ser Ser Glu Ile His Asn Thr Gly  
25 30 35 40  
Leu Thr Ile Leu His Gly Glu Lys Ser His Val Leu Gly Ser Gln Pro  
45 50 55  
Ile Leu Ala Lys Lys Lys Lys  
60

<210> 230  
<211> 54  
<212> PRT  
<213> Homo sapiens

<400> 230  
Ala Phe Val Trp Glu Pro Ala Met Val Arg Ile Asn Ala Leu Thr Ala  
1 5 10 15  
Ala Ser Glu Ala Ala Cys Leu Ile Val Ser Val Asp Glu Thr Ile Lys  
20 25 30  
Asn Pro Arg Ser Thr Val Asp Ala Pro Thr Ala Ala Gly Arg Gly Arg  
35 40 45  
Gly Arg Gly Arg Pro His  
50

<210> 231  
<211> 210  
<212> PRT  
<213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> -14...-1

<400> 231  
 Met Leu Thr Leu Leu Gly Leu Ser Phe Ile Leu Ala Gly Leu Ile Val  
       -10            -5            1  
 Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr  
       5              10            15  
 Arg Gly Glu Met Cys Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu  
       20            25            30  
 Arg Gly Gly Glu Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile  
       35            40            45            50  
 Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe  
       55            60            65  
 Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met  
       70            75            80  
 Thr Ala Tyr Leu Asp Leu Leu Leu Gly Ile Cys Tyr Leu Met Pro Leu  
       85            90            95  
 Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe Gly  
       100           105          110  
 Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val Arg Glu  
       115           120          125          130  
 Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn Leu Gly Ile  
       135           140          145  
 Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe Arg Leu Arg Arg  
       150           155          160  
 Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala Ile Asp Lys Cys Trp  
       165           170          175  
 Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val Glu Thr Lys Ile Cys  
       180           185          190  
 Gln Glu  
 195

<210> 232  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 232  
 Met Gly Cys Val Phe Gln Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile  
       1            5            10            15  
 Asp Trp Thr Leu Ser Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu  
       20           25            30  
 Tyr Tyr Tyr Ser Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg  
       35           40            45  
 Val His Leu Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu  
       50           55            60  
 Gln Asp Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg  
       65           70            75            80  
 Leu Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val  
       85           90            95  
 Leu Pro Glu Glu Pro Lys Gly Thr Gln Met Leu Thr  
       100          105

<210> 233  
 <211> 43

<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -18...-1

<400> 233  
Met Ser Ser Gly Arg Leu Arg Trp Leu Met Pro Val Ile Pro Ala Leu  
-15 -10 -5  
Trp Gly Ala Glu Lys Gly Glu Ser Pro Glu Val Ser Ser Phe Glu Thr  
1 5 10  
Arg Leu Ala Asn Met Ala Lys Pro Cys Leu Tyr  
15 20 25

<210> 234  
<211> 36  
<212> PRT  
<213> Homo sapiens

<400> 234  
Met Ser Ala Arg Ile Pro Phe Tyr Lys Asp Thr Ser Gln Ile Arg Leu  
1 5 10 15  
Gly Ser Thr Ile Ile Pro His Phe Asn Leu Ile Thr Phe Val Lys Thr  
20 25 30  
Phe Phe Gln Ile  
35

<210> 235  
<211> 307  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -13...-1

<400> 235  
Met Leu Ala Val Ser Leu Thr Val Pro Leu Leu Gly Ala Met Met Leu  
-10 -5 1  
Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro  
5 10 15  
Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu  
20 25 30 35  
Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile  
40 45 50  
Gly Asp Val Met Phe Thr Gly Thr Ala Asp Gly Arg Val Val Lys Leu  
55 60 65  
Glu Asn Gly Glu Ile Glu Thr Ile Ala Arg Phe Gly Ser Gly Pro Cys  
70 75 80  
Lys Thr Arg Asp Asp Glu Pro Val Cys Gly Arg Pro Leu Gly Ile Arg  
85 90 95  
Ala Gly Pro Asn Gly Thr Leu Phe Val Ala Asp Ala Cys Lys Gly Leu  
100 105 110 115  
Phe Glu Val Asn Pro Trp Lys Arg Glu Val Lys Leu Leu Ser Ser  
120 125 130  
Glu Thr Pro Ile Glu Gly Lys Asn Met Ser Phe Val Asn Asp Leu Thr  
135 140 145

Val Ser Gln Asp Gly Arg Lys Ile Tyr Phe Thr Asp Ser Ser Ser Lys  
 150 155 160  
 Trp Gln Arg Arg Asp Tyr Leu Leu Leu Val Met Glu Gly Thr Asp Asp  
 165 170 175  
 Gly Arg Leu Leu Glu Tyr Asp Thr Val Thr Arg Glu Val Lys Val Leu  
 180 185 190 195  
 Leu Asp Gln Leu Arg Phe Pro Asn Gly Val Gln Leu Ser Pro Ala Glu  
 200 205 210  
 Asp Phe Val Leu Val Ala Glu Thr Thr Met Ala Arg Ile Arg Arg Val  
 215 220 225  
 Tyr Val Ser Gly Leu Met Lys Gly Gly Ala Asp Leu Phe Val Glu Asn  
 230 235 240  
 Met Pro Gly Phe Pro Asp Asn Ile Arg Pro Ser Ser Gly Gly Tyr  
 245 250 255  
 Trp Val Gly Met Ser Thr Ile Arg Pro Asn Pro Gly Phe Ser Met Leu  
 260 265 270 275  
 Asp Phe Leu Ser Glu Arg Pro Trp Ile Lys Arg Met Ile Phe Lys Ala  
 280 285 290  
 Lys Lys Lys

<210> 236  
<211> 106  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -32..-1

<400> 236  
 Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu  
 -30 -25 -20  
 Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly  
 -15 -10 -5  
 Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met  
 1 5 10 15  
 Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu  
 20 25 30  
 Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn  
 35 40 45  
 Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Arg  
 50 55 60  
 Asn Pro Glu Ser Leu Lys Thr Lys Thr Thr  
 65 70

<210> 237  
<211> 42  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -19..-1

<400> 237  
 Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe  
 -15 -10 -5  
 Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro

1 5 10  
Gln Leu Ser Asp Lys Val His Asn Asp Ile  
15 20

<210> 238  
<211> 117  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -20..-1

<400> 238  
Met Asp Asn Arg Phe Ala Thr Ala Phe Val Ile Ala Cys Val Leu Ser  
-20 -15 -10 -5  
Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile Gly Thr Asp Phe Trp  
1 5 10  
Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser Ser Asp Leu Asn Lys  
15 20 25  
Ser Ile Trp Asp Glu Phe Ile Ser Asp Glu Ala Asp Glu Lys Thr Tyr  
30 35 40  
Asn Asp Ala Leu Phe Arg Tyr Asn Gly Thr Val Gly Leu Trp Gly Arg  
45 50 55 60  
Cys Ile Thr Ile Pro Lys Asn Met His Trp Tyr Ser Pro Pro Glu Arg  
65 70 75  
Thr Gly Ile Ser Leu Ile Leu Thr Ser Val Phe Phe Thr Trp Leu Ile  
80 85 90  
Ile Asp Lys Thr Thr  
95

<210> 239  
<211> 178  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> -37..-1

<400> 239  
Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe  
-35 -30 -25  
Gln His Xaa Xaa Ala Xaa Xaa Leu Leu Val Phe Asn Phe Leu Leu Ile  
-20 -15 -10  
Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe  
-5 1 5 10  
Leu His Glu Thr Gly Gly Ala Met Val Tyr Gly Leu Ile Met Gly Leu  
15 20 25  
Ile Ser Arg Tyr Ala Thr Ala Pro Thr Asp Ile Glu Ser Gly Thr Val  
30 35 40  
Cys Asp Cys Val Lys Leu Thr Phe Ser Pro Pro Thr Leu Leu Val Asn  
45 50 55  
Val Thr Asp Gln Val Tyr Glu Tyr Lys Tyr Lys Arg Glu Ile Ser Gln  
60 65 70 75  
His Asn Ile Asn Pro His Gln Gly Asn Ala Ile Leu Glu Lys Met Thr  
80 85 90  
Phe Asp Pro Glu Ile Phe Phe Asn Val Leu Leu Pro Pro Ile Ile Phe

<210> 240  
<211> 126  
<212> PRT  
<213> *Homo sapiens*

<220>  
<221> SIGNAL  
<222> -27..-1

<400> 240  
 Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly Val Val  
       -25            -20                  -15  
 Val Leu Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr Glu Ser  
       -10              -5                  1                  5  
 Met Cys Ala Leu Val Thr Phe Phe Ile Leu Leu Leu Ile Phe Ile  
       10                 15                 20  
 Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr Met Ala  
       25                 30                 35  
 Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys Asp Tyr  
       40                 45                 50  
 Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met Lys Gly  
       55                 60                 65  
 Leu Lys Cys Arg Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro  
       70                 75                 80                 85  
 Tyr Phe Lys Met His Lys Pro Val Thr Met Lys Lys Lys Lys  
       90                 95

<210> 241  
<211> 174  
<212> PRT  
<213> *Homo sapiens*

<220>  
<221> SIGNAL  
<222> -115...-1

<400> 241  
 Met Arg Trp Ser Cys Glu His Leu Val Met Val Trp Ile Asn Ala Phe  
 -115 -110 -105 -100  
 Val Met Leu Thr Thr Gln Leu Leu Pro Ser Lys Tyr Cys Asp Leu Leu  
 -95 -90 -85  
 His Lys Ser Ala Ala His Leu Gly Lys Trp Gln Lys Leu Glu His Gly  
 -80 -75 -70  
 Ser Tyr Ser Asn Ala Pro Gln His Ile Trp Ser Glu Asn Thr Ile Trp  
 -65 -60 -55  
 Pro Gln Gly Val Leu Val Arg His Ser Arg Cys Leu Tyr Arg Ala Met  
 -50 -45 -40  
 Gly Pro Tyr Asn Val Ala Val Pro Ser Asp Val Ser His Ala Arg Phe  
 -35 -30 -25 -20  
 Tyr Phe Leu Phe His Arg Pro Leu Arg Leu Leu Asn Leu Leu Ile Leu

-15	-10	-5
Ile Glu Gly Gly Val Val Phe Tyr Gln Leu Tyr Ser Leu Leu Arg Ser		
1	5	10
Glu Lys Trp Asn His Thr Leu Ser Met Ala Leu Ile Leu Phe Cys Asn		
15	20	25
Tyr Tyr Val Leu Phe Lys Leu Leu Arg Asp Arg Ile Val Leu Gly Arg		
30	35	40
Ala Tyr Ser Tyr Pro Leu Asn Ser Tyr Glu Leu Lys Ala Asn		
50	55	

<210> 242  
<211> 896  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 18..173

<221> sig\_peptide  
<222> 18..77  
<223> Von Heijne matrix  
score 6.5  
seq GLCVLQLTAVTS/AF

<221> polyA\_signal  
<222> 864..869

<221> polyA\_site  
<222> 882..893

<400> 242 aaccttcaca gtgtgag atg cct agt gtg aac aat gct gga tta tgt gtc Met Pro Ser Val Asn Ser Ala Gly Leu Cys Val -20 -15 -10 ttg cag ttg aca acg gca gtr acc agt gcc ttt tta cta gca aaa gtg Leu Gln Leu Thr Thr Ala Val Thr Ser Ala Phe Leu Leu Ala Lys Val -5 1 5 aat cct ttc gaa rct ttt ctc tca agg ggc ttt tgg cta tgt gct gcc Asn Pro Phe Glu Xaa Phe Leu Ser Arg Gly Phe Trp Leu Cys Ala Ala 10 15 20 cat cat ttc att cat cct tgc ctg gat tgagacgtgt tcctgattca His His Phe Ile His Pro Cys Leu Asp 25 30 aagtgttacc tcaagaagca gaagaagaaa acagactcct gatagttcag gatgtttcag agaggcagc acttataacct ggtggcttt ctgatggta gttttattcc cctcttgc ccgaagcagg atctgaagaaa gctgaagaaa aacaggacag tgagaaacca cttttagaac tatgagtact acttttgtt aatgtgaaaa accctcacag aaagtcatcg aggcaaaaag aggcaggcag tggagtctcc ctgtcgacag taaagttgaa atggtgacgt ccactgctgg ctttattgaa cagctaataa agatttattt attgttaatac ctcacagacg ttgtaccata tccatgcaca ttttagttcc tgctgtggc tggtaaggta atgtcatgat tcatttc ttcagtgaga ctgagcctga tggatggaa aataggtgaa gaaagtctt tgctgtattc ctaatcaaaa gacttaatat attgaagtaa cacttttta gtaagcaaga tacctttta tttcaattca cagaatggaa ttttttttgc tcatgtctca gatttatttt gtatttctt tttaacactc tacatttccc ttgtttttta actcatgcac atgtgcttt tgtaacgttt taaaaaagtgt aataaaatct gacatgtcaa araaaaaaaaa mcy	50  98  146  193  253 313 373 433 493 553 613 673 733 793 853 896
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<210> 243

<211> 851  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 17..595

<221> sig\_peptide  
 <222> 17..85  
 <223> Von Heijne matrix  
 score 3.70000004768372  
 seq FLPPLXRAFACRG/CQ

<221> polyA\_signal  
 <222> 820..825

<221> polyA\_site  
 <222> 840..851

<400> 243			
aaggggggcgt ggggcc atg gtg gtc ttg cgg gcg ggg aag aag acc ttt ctc		52	
Met Val Val Leu Arg Ala Gly Lys Lys Thr Phe Leu			
-20	-15		
ccc cct ctm wgc cgc gcc ttc gcc tgc cgc ggc tgt caa ctc gct ccg		100	
Pro Pro Leu Xaa Arg Ala Phe Ala Cys Arg Gly Cys Gln Leu Ala Pro			
-10	-5	1	5
gag cgc ggc gcc gag cgc agg gat aca gcg ccc agc ggg gtc tca aga		148	
Glu Arg Gly Ala Glu Arg Arg Asp Thr Ala Pro Ser Gly Val Ser Arg			
10	15	20	
tcc tgc cct cca aga aag tct tgc cat gat tgg ata gga ccc cca gat		196	
Phe Cys Pro Pro Arg Lys Ser Cys His Asp Trp Ile Gly Pro Pro Asp			
25	30	35	
aaa tat tca aac ctt cga cct gtt cac ttt tac ata cct gaa aat gaa		244	
Lys Tyr Ser Asn Leu Arg Pro Val His Phe Tyr Ile Pro Glu Asn Glu			
40	45	50	
tct cca ttg gaa caa aag ctt aga aaa tta aga caa gaa aca caa gaa		292	
Ser Pro Leu Glu Gln Lys Leu Arg Lys Leu Arg Gln Glu Thr Gln Glu			
55	60	65	
tgg aat caa cag ttc tgg gca aac cag aat ttg act ttt agt aag gaa		340	
Trp Asn Gln Gln Phe Trp Ala Asn Gln Asn Leu Thr Phe Ser Lys Glu			
70	75	80	85
aaa gaa gaa ttt att cac tca aga cta aaa act aaa ggc ctg ggc ctg		388	
Lys Glu Glu Phe Ile His Ser Arg Leu Lys Thr Lys Gly Leu Gly Leu			
90	95	100	
aga act gaa tca ggt cag aaa gca aca ttg aat gca gaa gaa atg gcg		436	
Arg Thr Glu Ser Gly Gln Lys Ala Thr Leu Asn Ala Glu Glu Met Ala			
105	110	115	
gac ttc tac aag gaa ttt tta agt aaa aat ttt cag aag cac atg tat		484	
Asp Phe Tyr Lys Glu Phe Leu Ser Lys Asn Phe Gln Lys His Met Tyr			
120	125	130	
tat aac aga gat tgg tac aag cgc aat ttt gcc atc acc ttc ttc atg		532	
Tyr Asn Arg Asp Trp Tyr Lys Arg Asn Phe Ala Ile Thr Phe Phe Met			
135	140	145	
gga aaa gtg gcc ctg gaa agg att tgg aac aag ctt aaa cag aaa caa		580	
Gly Lys Val Ala Leu Glu Arg Ile Trp Asn Lys Leu Lys Gln Lys Gln			
150	155	160	165
aag aag agg agc aac taggagtcca ctctgaccac gccagagtcc aggtttccac		635	
Lys Lys Arg Ser Asn			
170			
aggaagcara tggagctctt ttcacagggg ctctgagaaaa aactggagct gatctcaaga		695	
agccccacat cttctaagg ggccccatgg cctgtttggg ggcaggtag gtcctgggc		755	

actgtgggcc gcctgcctgc tcatgtggc tctaggccag cttgttgtca cgtacgtggt 815  
 gtgaaataaa gcccaagcac tggaaaaaaa aaaaaaa 851

<210> 244  
 <211> 495  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 89..334

<221> sig\_peptide  
 <222> 89..130  
 <223> Von Heijne matrix  
 score 3.5999990463257  
 seq AFTLXSLLQAAALL/CV

<221> polyA\_signal  
 <222> 462..467

<221> polyA\_site  
 <222> 484..495

<400> 244  
 agtaggaasg cgcccgscggc ggagggcgcca cgtcccttgc sgccggcgaa gagamatcgc 60  
 ttggacttcg gggcgccctc ggacggcc atg gcc ttt acc ctg tas tca ctg 112  
 Met Ala Phe Thr Leu Xaa Ser Leu  
 -10  
 ctg cag gca gcc ctg ctc tgc gtc aac gcc atc gca gtg ctg cac gag 160  
 Leu Gln Ala Ala Leu Leu Cys Val Asn Ala Ile Ala Val Leu His Glu  
 -5 1 5 10  
 gag cga ttc ctc aag aac att ggc tgg gga aca gac cag gga att ggt 208  
 Glu Arg Phe Leu Lys Asn Ile Gly Trp Gly Thr Asp Gln Gly Ile Gly  
 15 20 25  
 gga ttt gga gaa gag ccg gga att aaa tca sag sta atg avs ctt att 256  
 Gly Phe Gly Glu Pro Gly Ile Lys Ser Xaa Xaa Met Xaa Leu Ile  
 30 35 40  
 cga tct gta aga acc gtg atg aga gtg cca ttg ata ata gta aac tca 304  
 Arg Ser Val Arg Thr Val Met Arg Val Pro Leu Ile Ile Val Asn Ser  
 45 50 55  
 att gca att gtg tta ctt tta ttt gga tgaatwtcat tggagaaaaat 354  
 Ile Ala Ile Val Leu Leu Leu Phe Gly  
 60 65  
 ggakactcag aaraggacat gccaktaraa kttattactt tggtcattat tggaatattt 414  
 atatcttagc tggctgacct tgcacttgc aaaaatgtaa agctgaaaat aaaaccaggg 474  
 tttctattta aaaaaaaaaa a 495

<210> 245  
 <211> 884  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 21..614

<221> sig\_peptide

<222> 21..83  
 <223> Von Heijne matrix  
 score 10  
 seq LWALAMVTRPASA/AP

<221> polyA\_signal  
 <222> 849..854

<221> polyA\_site  
 <222> 873..884

<400> 245

aataaccttag accctcagtc atg cca gtg cct gct ctg tgc ctc tgg gcc	53		
Met Pro Val Pro Ala Leu Cys Leu Leu Trp Ala			
-20	-15		
ctg gca atg gtg acc cgg cct gcc tca gcg gcc ccc atg ggc ggc cca	101		
Leu Ala Met Val Thr Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro			
-10	-5	1	5
gaa ctg gca cag cat gag gag ctg acc ctg ctc ttc cat ggg acc ctg	149		
Glu Leu Ala Gln His Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu			
10	15	20	
cag ctg ggc cag gcc ctc aac ggt gtg tac agg acc acg gag gga cgg	197		
Gln Leu Gly Gln Ala Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Arg			
25	30	35	
ctg aca aag gcc agg aac agc ctg ggt ctc tat ggc cgc aca ata gaa	245		
Leu Thr Lys Ala Arg Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu			
40	45	50	
ctc ctg ggg cag gag gtc agc cgg ggc cgg gat gca gcc cag gaa ctt	293		
Leu Leu Gly Gln Glu Val Ser Arg Gly Arg Asp Ala Ala Gln Glu Leu			
55	60	65	70
cgg gca agc ctg ttg gaa act car atg gag gag gat att ctg cas ctg	341		
Arg Ala Ser Leu Leu Glu Thr Gln Met Glu Glu Asp Ile Leu Xaa Leu			
75	80	85	
cag gca rag gcc aca gct gag gtg ctg ggg gag gtg gcc cag gca car	389		
Gln Ala Xaa Ala Thr Ala Glu Val Leu Gly Glu Val Ala Gln Ala Gln			
90	95	100	
aag gtg cta cgg gac agc gtg cag cgg cta daa ktc cag ctg arg asc	437		
Lys Val Leu Arg Asp Ser Val Gln Arg Leu Xaa Xaa Gln Leu Xaa Xaa			
105	110	115	
gcc tgg ctg ggc cct gcc tac cga aaa ttt gar gtc tta aag gcy ccc	485		
Ala Trp Leu Gly Pro Ala Tyr Arg Lys Phe Glu Val Leu Lys Ala Pro			
120	125	130	
cck gam aar car aac cac atc cta tgg gcc ctc aca ggc cac gtg cak	533		
Pro Xaa Lys Gln Asn His Ile Leu Trp Ala Leu Thr Gly His Val Xaa			
135	140	145	150
cgg car arg cgg gar atg gtg gca cag cag cwt ckg ctg cna car atc	581		
Arg Gln Xaa Arg Glu Met Val Ala Gln Gln Xaa Xaa Leu Xaa Gln Ile			
155	160	165	
cag gar aaa ctc cac aca gcg gcg ctc cca gcc tgaatctgcc tggatggAAC	634		
Gln Glu Lys Leu His Thr Ala Ala Leu Pro Ala			
170	175		
tgaggaccAA tcatgctgca aggaacactt ccacggcccc tgaggcccc gtgcaggAG	694		
gagctgcctg ttcaactggGA tcagccaggG cgccggggCC cacttctgag cacagAGcar	754		
agacagacGC aggcggggAC aaaggcAGAG gatgtAGCCC cattggggAG gggTggAGGA	814		
aggacatgTA ccctttcatr mctacacACC cctcattaaa gcavagtCGT ggcATctCAA	874		
aaaaaaaaaaaa	884		

<210> 246  
 <211> 897  
 <212> DNA



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<210> 247
<211> 518
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 74..397

<221> sig_peptide
<222> 74..127
<223> Von Heijne matrix
    score 7.69999980926514
    seq LLLLPVLGLLVSS/KT

<221> polyA_signal
<222> 472..477

<221> polyA_site
<222> 507..518

<400> 247
aaagaaaagag ctgcsgtgca ggaattcgtg tgccggattt ggtagctga gcccaccgag      60
aggcgccctgc agg atg aaa gct ctc tgt ctc ctc ctc ctc cct gtc ctg      109
    Met Lys Ala Leu Cys Leu Leu Leu Leu Pro Val Leu
    -15           -10
ggg ctg ttg gtg tct agc aag acc ctg tgc tcc atg gaa gaa gcc atc      157
Gly Leu Leu Val Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala Ile
    -5           1           5           10
aat gag agg atc cag gag gtc gcc ggc tcc cta ata ttt agg gca ata      205
Asn Glu Arg Ile Gln Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ile
    15           20           25
agc agc att ggc cga ggg agc gag agc gtc acc tcc agg ggg gac ctg      253
Ser Ser Ile Gly Arg Gly Ser Glu Ser Val Thr Ser Arg Gly Asp Leu
    30           35           40
gct act tgc ccc cga ggc ttc gcc gtc acc ggc tgc act tgt ggc tcc      301
Ala Thr Cys Pro Arg Gly Phe Ala Val Thr Gly Cys Thr Cys Gly Ser
    45           50           55
gcc tgt ggc tcg tgg gat gtg cgc gcc gag acc aca tgt cac tgc cag      349
Ala Cys Gly Ser Trp Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln
    60           65           70
tgc gcg ggc atg gac tgg acc gga gcg cgc tgc tgt cgt gtg cag ccc      397
Cys Ala Gly Met Asp Trp Thr Gly Ala Arg Cys Cys Arg Val Gln Pro
    75           80           85           90
tgaggtcgcg cgcaagcgcgt gcacagcgcg ggcggaggcg gctccaggc cgaggagggtt      457
gcgggggagc tggaaataaa cctggagatg atgatgatga tggatggaa aaaaaaaaaa
a

<210> 248
<211> 350
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 51..242

<221> sig_peptide
<222> 51..116
<223> Von Heijne matrix

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score 6.5  
 seq SCLCPALFPGTSS/FI

<221> polyA\_signal  
<222> 319..324

<221> polyA\_site  
<222> 339..350

<400> 248  
acgtcattcc aaaaccacac ctttgc aaag ctttgtactc cgcacccca gatg atc 56  
Met Ile  
tcc agg cag ctc aga tct ctt tcc tgc ctt tgc cct gca ctg ttc ccc 104  
Ser Arg Gln Leu Arg Ser Leu Ser Cys Leu Cys Pro Ala Leu Phe Pro  
-20 -15 -10 -5  
ggta ctttcc tttt att gta gca ctc agc tcc cca gcc gat ctg tac 152  
Gly Thr Ser Ser Phe Ile Val Ala Leu Ser Ser Pro Ala Asp Leu Tyr  
1 5 10  
atc cct cav agg cas cga tct gat gaa ttg gtt ttt gaa tcc car aaa 200  
Ile Pro Xaa Arg Xaa Arg Ser Asp Glu Leu Val Phe Glu Ser Gln Lys  
15 20 25  
ggg tct gcc atg gag ttg gca gtc atc acg gta rat ggc gta 242  
Gly Ser Ala Met Glu Leu Ala Val Ile Thr Val Xaa Gly Val  
30 35 40  
tgat tttgct gaattttaaa taaaatgaaa accataaaatt acatratgct tttattgach 302  
cttgacma ctggcctaaataaaaaractct gactccaaaa aaaaaaaaaa 350

<210> 249  
<211> 996  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 111..191

<221> sig\_peptide  
<222> 111..155  
<223> Von Heijne matrix  
score 5.80000019073486  
seq FLXLMTLTTHVHS/SA

<221> polyA\_signal  
<222> 965..970

<221> polyA\_site  
<222> 986..996

<400> 249  
atccgataca gaacatgcag taatgtggac tgcccaccag aagcaggta tttccgagct 60  
cagcaatgct cagctataa tgatgtcaag caccatggcc agtttatga atg ggy 116  
Met Gly  
-15  
ttc ctg wgt cta atg acc ctg aca acc cat gtt cac tca agt gcc aag  
Phe Leu Xaa Leu Met Thr Leu Thr His Val His Ser Ser Ala Lys  
-10 -5 1  
cca aat gaa caa ccc tgg ttg ttg aac tagcaccta ggtcttarat 164  
Pro Asn Glu Gln Pro Trp Leu Leu Asn  
5 10  
ggtagcggtt gctatacaga atctttggat atgtgcatac gtggttatg ccaaattgtt 211  
271

ggctgcgatc	accagctggg	aaggcacccgtc	aaggaarata	actgtgggg	ctgcaacrga	331
natgggtcca	cctgccggct	ggtccggaggg	cartataaat	cccakctctc	cgcaaccaaa	391
tcratgata	ctgtggttgc	aattccctat	ggaagtakac	atattcgct	tgtctaaaa	451
ggtcctgatc	acttatatatct	ggaarccawa	accctccagg	ggactaawgg	tgaaaacagt	511
ctcasctcca	caggaacttt	ccttggac	aattcttagt	tggacttcca	gaawtttcca	571
gacwdagaga	tactgagaat	ggctggacca	ctcacagcag	atttcattgt	caawattcgt	631
aactcgggct	ccgctgacag	tacagtccag	kkcatcttct	atcaacccat	catccaccga	691
tggagggara	cggatttctt	tccttgctca	gcaacctgt	gaggaggtt	tcagctgaca	751
tcggctgagt	gctacgatct	gaggagcaac	cgtgtggtt	ctgaccaata	ctgtcactat	811
tacccagaga	acatcaaacc	caaacccaag	cttcaggagt	gcaacttgg	tccttgtcca	871
gccaggtcag	tcaaatttgc	tagttcattt	gtcataaaca	taactcaagt	tccaaatagg	931
ttatTTaaat	taaaatgaaa	cgttttaatt	aaaaataaaa	tgaaattaaa	catcaaaaaa	991
aaaaaa						996

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                                         Met Ser Pro Ser
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ggc cgc ctg tgt ctt ctc acc atc gtt ggc ctg att ctc ccc acc aga
Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile Leu Pro Thr Arg    104
-15                               -10                           -5
gga cag acg ttg aaa gat acc acg tcc agt tct tca gca gac tca act
Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser Ala Asp Ser Thr   152
-15
1          5           10           15
atc atg gac att cag gtc ccg aca cga gcc cca gat gca gtc tac aca
Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp Ala Val Tyr Thr   200
-20                               25           30
gaa ctc cag ccc acc tct cca acc cca acc tgg cct gct gat gaa aca
Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro Ala Asp Glu Thr   248
-35
35           40           45
ccca caa ccc cag acc cag acc cag caa ctg gaa gga acg gat ggg cct
Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly Thr Asp Gly Pro   296
-50
50           55           60
cta gtg aca gat cca gag aca cac wak agc mcc aaa gca gct cat ccc
Leu Val Thr Asp Pro Glu Thr His Xaa Ser Xaa Lys Ala Ala His Pro   344
-65
65           70           75
act gat gac acc acg acg ctc tct gag aga cca tcc cca agc aca kac
Thr Asp Asp Thr Thr Leu Ser Glu Arg Pro Ser Pro Ser Thr Xaa     392
-80
80           85           90           95

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gtc cat dac aga ccb cba kda ccc tca akc cat ctg gtt etc atg agg	440
Val His Xaa Arg Pro Xaa Xaa Pro Ser Xaa His Leu Val Phe Met Arg	
100 105 110	
atg acc cct tct tct atg atg aac aca ccc tcc gga aac sgg ggc tgt	488
Met Thr Pro Ser Ser Met Met Asn Thr Pro Ser Gly Asn Xaa Gly Cys	
115 120 125	
tgg tcg cag ctg tgc tgt tca tca cag gca tca tca tcc tca cca gtg	536
Trp Ser Gln Leu Cys Cys Ser Ser Gln Ala Ser Ser Ser Pro Val	
130 135 140	
gca agt gca ggc agc tgt ccc ggt tat gcc gga atc att gca ggt gag	584
Ala Ser Ala Gly Ser Cys Pro Gly Tyr Ala Gly Ile Ile Ala Gly Glu	
145 150 155	
tcc atc aga aac agg agc tgacaacctg ctgggcaccc gaagaccaag	632
Ser Ile Arg Asn Arg Ser	
160 165	
ccccctgcca gtcaccgtg cccagcctcc tgcatccccct cgaagagcct ggccagagag	692
ggaagacaca gatgatgaag ctggagccag ggctgccgt ccgagtctcc tacctccccc	752
aaccctgccc gcccctgaag gctacctggc gccttgggg ctgtccctca agttatctcc	812
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Met Glu Thr Gly Ala Leu Arg Arg Pro Gln	
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ctt ctc ccg ttg ctg ctg ctc tgc ggc cct tcc cag gat caa tgc	101
Leu Leu Pro Leu Leu Leu Leu Cys Gly Pro Ser Gln Asp Gln Cys	
-15 -10 -5	
cga cct gta ctc cag aat ctg ttg cag agc cca ggc ttg aca tgg agc	149
Arg Pro Val Leu Gln Asn Leu Gln Ser Pro Gly Leu Thr Trp Ser	
1 5 10 15	
ttg gaa gtg ccc act ggg aga gaa gga aag gaa ggt ggg gat cgg gga	197
Leu Glu Val Pro Thr Gly Arg Glu Gly Lys Glu Gly Asp Arg Gly	
20 25 30	
cca ggg cta akt ggg gcc act cca gcc agg agc cct cag ggc aag gag	245
Pro Gly Leu Xaa Gly Ala Thr Pro Ala Arg Ser Pro Gln Gly Lys Glu	
35 40 45	
atg ggg aga caa agg acc aga aag gtg aag ggc cct gct tgg akt cac	293
Met Gly Arg Gln Arg Thr Arg Lys Val Lys Gly Pro Ala Trp Xaa His	
50 55 60	

aca gca aat cag gaa cta aac agg atg agg tct ctg tct tct ggc tcc	341
Thr Ala Asn Gln Glu Leu Asn Arg Met Arg Ser Leu Ser Ser Gly Ser	
65 70 75 80	
gtg cca gtg ggg cat ctg gag ggt ggc acg gtc aag ctt cag aag gac	389
Val Pro Val Gly His Leu Glu Gly Gly Thr Val Lys Leu Gln Lys Asp	
85 90 95	
acg ggc ctc cat tcc tgc ara gat ggt atg gct tct ctt gaa ggg acg	437
Thr Gly Leu His Ser Cys Xaa Asp Gly Met Ala Ser Leu Glu Gly Thr	
100 105 110	
cca gct tca gtc ctg gct gat gct tgc cca gga ttc cat gat gtg aan	485
Pro Ala Ser Val Leu Ala Asp Ala Cys Pro Gly Phe His Asp Val Xaa	
115 120 125	
gtt car arg gcc cta ttt ggg tta agt ggg ana rta ctg tgg ctg aaa	533
Val Gln Xaa Ala Leu Phe Gly Leu Ser Gly Xaa Xaa Leu Trp Leu Lys	
130 135 140	
acc cac ttc tgc ctt tct att ana ctt taaataaaact ctgaaracct	580
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Met Ala Thr	
-55	
aca gtc cct gat ggt tgc cgc aat ggc ctg aaa tcc aag tac tac aga	165
Thr Val Pro Asp Gly Cys Arg Asn Gly Leu Lys Ser Lys Tyr Tyr Arg	
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ctt tgt gat aag gct gaa gct tgg ggc atc gtc cta gaa acg gtg gcc	213
Leu Cys Asp Lys Ala Glu Ala Trp Gly Ile Val Leu Glu Thr Val Ala	
-35 -30 -25	
aca gcc ggg gtt gtg acc tcg gtg gcc ttc atg ctg act ctc ccg atc	261
Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr Leu Pro Ile	
-20 -15 -10 -5	
ctc gtc tgc aag gtg cag gac tcc aac agg cga aaa atg ctg cct act	309
Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met Leu Pro Thr	
1 5 10	
cag ttt ctc ttc ctc ctg ggt gtg ttg ggc atc ttt ggc ctc acc ttc	357
Gln Phe Leu Phe Leu Leu Gly Val Leu Gly Ile Phe Gly Leu Thr Phe	
15 20 25	
gcc ttc atc atc gga ctg gac ggg agc aca ggg ccc aca cgc ttc ttc	405
Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr Arg Phe Phe	

30	35	40	
ctc ttt ggg atc ctc ttt tcc atc tgc ttc tcc tgc ctg ctg gct cat			453
Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu Leu Ala His			
45	50	55	60
gct gtc agt ctg acc aag ctc gtc cg <sup>g</sup> ggg agg aaa gcc cct ttc cct			501
Ala Val Ser Leu Thr Lys Leu Val Arg Gly Arg Lys Ala Pro Phe Pro			
65	70	75	
gtt ggt gat tct ggg tct ggc cgt ggg ctt cag cct agt cca gga tgt			549
Val Gly Asp Ser Gly Ser Gly Arg Gly Leu Gln Pro Ser Pro Gly Cys			
80	85	90	
tat cgc tat tgaatatatt gtcctgacca tgaataggac caacgtcaat			598
Tyr Arg Tyr			
95			
gtcttttctg agctttccgc tcctcgctgc aatgaaaaact ttgtccctcct gctcacctac			658
ktcctttctt tcatggcgct gaccccttc wtgtccctc tCACCTTCTG tggtkccttc			718
acgggcttggaa avagacatgg ggcccacatc tacctcasga tgctcskctc cattgccatc			778
tgggtggcct ggatcacccct gctcatgctt cctgactttg accgcrgggtg ggatgacacc			838
atcmcarct ccgccttggs trcsaatggc tgggtgttcc tgggtggctta tgtagtccc			898
gagttttggc tgctcacaaa gcaackaaac cccatggatt atcctgttga ggatgcttcc			958
tgtaaacctc aactcgtgaa gaagagctat ggtgtgrga acagagccta skctcaagag			1018
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<221> polyA\_site  
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ccgcgcgcgt ttccgttattg gttgtgggtg gctacctctt cgttctgtt ggccgcgtagt			120
gagcaag atg ctg agc aag ggt ctg aag cgg aaa cgg gag gag gag			169
Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu			
-30	-25	-20	
gag aag gaa cct ctg gca gtc gac tcc tgg tgg cta gat cct ggc cac			217
Glu Lys Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His			
-15	-10	-5	
gca gcg gtg gca cag gca ccc ccg gcc gtg gcc tct agc tcc ctc ttt			265
Ala Ala Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe			
1	5	10	15
gac ctc tca gtg ctc aag ctc cac cac agc ctg cag vrr agt rag ccg			313
Asp Leu Ser Val Leu Lys Leu His His Ser Leu Gln Xaa Ser Xaa Pro			
20	25	30	
gac ctg cgg cac ctg gtg ctg gtc atr aac act ctg cgg cgc atc cag			361

Asp Leu Arg His Leu Val Leu Val Xaa Asn Thr Leu Arg Arg Ile Gln			
35	40	45	
gca tcc atg gca ccc gcg gct gcc ctg cca cct gtg cct acc cca cct			409
Ala Ser Met Ala Pro Ala Ala Leu Pro Pro Val Pro Thr Pro Pro			
50	55	60	
gca gcc ccc ant gtg gct gac aac tta ctg gca agc tcg gac gct gcc			457
Ala Ala Pro Xaa Val Ala Asp Asn Leu Leu Ala Ser Ser Asp Ala Ala			
65	70	75	
ctt tca gcc tcc atg gcc arm ctc ctg gar gac ctc agc cac att gag			505
Leu Ser Ala Ser Met Ala Xaa Leu Leu Glu Asp Leu Ser His Ile Glu			
80	85	90	95
ggc ctg agt cag gct ccc caa ccc ttg gca gac gag ggg cca cca ggc			553
Gly Leu Ser Gln Ala Pro Gln Pro Leu Ala Asp Glu Gly Pro Pro Gly			
100	105	110	
cgt agc atc ggg gga wca ccg ccc amc ctg ggt gcc ttg gac ctg ctg			601
Arg Ser Ile Gly Gly Xaa Pro Pro Xaa Leu Gly Ala Leu Asp Leu Leu			
115	120	125	
ggc cca gcc act ggc tgt cta ctg gac aat ggg ctt gag ggc ctg ttt			649
Gly Pro Ala Thr Gly Cys Leu Leu Asp Asn Gly Leu Glu Gly Leu Phe			
130	135	140	
gag gat att gac acc tct atg tat gac aat gaa ctt tgg gca cca gcc			697
Glu Asp Ile Asp Thr Ser Met Tyr Asp Asn Glu Leu Trp Ala Pro Ala			
145	150	155	
tct gag ggc ctc aaa cca ggc cct gag gat ggg ccg ggc aag gag gaa			745
Ser Glu Gly Leu Lys Pro Gly Pro Glu Asp Gly Pro Gly Lys Glu Glu			
160	165	170	175
gct ccg gag ctg gac gag gcc gaa ttg gac tac ctc atg gat gtg ctg			793
Ala Pro Glu Leu Asp Glu Ala Glu Leu Asp Tyr Leu Met Asp Val Leu			
180	185	190	
gtg ggc aca cag gca ctg gag cga ccg ccg ggg cca ggg cgc			835
Val Gly Thr Gln Ala Leu Glu Arg Pro Pro Gly Pro Gly Arg			
195	200	205	
tgagccctcg tgctgaaatg gttgtctgg atctgaactg agcctgctgg ctggaccacac			895
tgtcctcgaa aagacacacgc tggctccct agtacagaga acagggtttg ggccactttg			955
gagagacaga atctagtccct gggcaacttc acatccgtcc tcctgtctca gggctggcag			1015
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ctggccctgg ggtcatagct tgggctgttc cttctctgat acgggaagag acccaatcag			1135
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atg gag act ttg tac cgt gtc ccg ttc tta gtg ctc gaa tgt ccc aac 106  
Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn  
-100 -95 -90 -85  
ctg aag ctg aag aag ccg ccc tgg ttg cac atg ccg tcg gcc atg act 154  
Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr  
-80 -75 -70  
gtg tat gct ctg gtg gtg tct tac ttc ctc atc acc gga gga ata 202  
Val Tyr Ala Leu Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile  
-65 -60 -55  
att tat gat gtt att gtt gaa cct cca agt gtc ggt tct atg act gat 250  
Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp  
-50 -45 -40  
gaa cat ggg cat cag agg cca gta gct ttc ttg gcc tac aga gta aat 298  
Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn  
-35 -30 -25  
gga caa tat att atg gaa gga ctt gca tcc agc ttc cta ttt aca atg 346  
Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met  
-20 -15 -10 -5  
gga ggt tta ggt ttc ata atc ctg gac gga tcg aat gca cca aat atc 394  
Gly Gly Leu Gly Phe Ile Ile Leu Asp Gly Ser Asn Ala Pro Asn Ile  
1 5 10  
cca aaa ctc aat aga ttc ctt ctt ctg ttc att gga ttc gtc tgg gtc 442  
Pro Lys Leu Asn Arg Phe Leu Leu Phe Ile Gly Phe Val Cys Val  
15 20 25  
cta twr agt ttt tkc ayg gct aga gta ttc atg aga atg aaa ctg ccg 490  
Leu Xaa Ser Phe Xaa Xaa Ala Arg Val Phe Met Arg Met Lys Leu Pro  
30 35 40  
ggc tat ctg atg ggt tagagtgcct ttgasaagaa atcagtggat actggatttg 545  
Gly Tyr Leu Met Gly  
45  
ctcctgtcaa wgaastttta aaggctgtmc caatcctcta atatgaaaatg tggaaaagaa 605  
tgaagagcag cagtaaaaaga aatatctagt gaaaaaacag gaagcgtatt gaagcttgg 665  
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ttccatatct acaactataa tatcaaataa agtgattatt ttttacaacc ctcttaacat 845  
tttttggaga tgacatttct gatttcaga aattaacata aaatccagaa gcaagattcc 905  
gtaagctgag aactctggac agttgatcag ctttacctat ggtgctttgc cttaactag 965  
agtgtgtgat ggttagattat ttcatatgtatg tatgtaaaac tttttcctga acaataagat 1025  
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<221> sig\_peptide  
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<221> polyA\_site  
<222> 807..818

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ctt acc cct tgc ctg act gta ccc cgt aga ccc ctg ttt ctc ctc ctg	96		
Leu Thr Pro Cys Leu Thr Val Pro Arg Arg Pro Leu Phe Leu Leu Leu			
-30	-25	-20	
cac ctg tgt ccc cat ctg ccc ttc ttg ttg ctc ctg tca tgt gtc ggg	144		
His Leu Cys Pro His Leu Pro Phe Leu Leu Leu Ser Cys Val Gly			
-15	-10	-5	
gkc www ccc tcc tgt ctg cct tcc tcc act tgt gtc agc ttg cat	192		
Xaa Xaa Pro Ser Cys Leu Pro Ser Ser Ser Thr Cys Val Ser Leu His			
1	5	10	15
ttt ttt att cct gac tgagtcacca caccctctc ccctgatcaa agggaatatk	247		
Phe Phe Ile Pro Asp			
20			
arttttaat ttggatcgac tgaggtgcca ggagaaaactg cagkcccagg tatccmvaca	307		
gccaccagga tggccctcg ccccccccccc accgcctctk ccccacctt tccaaacgtgt	367		
tgcatgtgg gaactggggg gtgtggggga agggggctgcc ggcttcttc aggangctga	427		
rgtttggarg caaaaatcaac ctgggaracc accccggccg cggccctca gtggacaggt	487		
gggargaaaa gaaaacttct taccttggar garggacatc ccgcttcctt atccttagct	547		
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cctcccggtt gggtaccagg gactgagttg gcctggggc cgtgtccaag gtgccaatga	727		
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score 4.80000019073486  
seq ILFCVGAVGACTL/SV

<221> polyA\_signal  
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<221> polyA\_site  
<222> 961..971

<400> 256

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-30	-25	-20
caa acc aat ctc att cta ttt tgt gtc ggt gct gtg ggc gcc tgt act	98	
Gln Thr Asn Leu Ile Leu Phe Cys Val Gly Ala Val Gly Ala Cys Thr		
-15	-10	-5
ctc tct gtc aca caa ccg tgg tac cta gaa gtg gac tac act cat gag	146	
Leu Ser Val Thr Gln Pro Trp Tyr Leu Glu Val Asp Tyr Thr His Glu		

1	5	10	15	
gcc gtc acc ata aag tgt acc ttc tcc gca acc gga tgc cct tct gag				194
Ala Val Thr Ile Lys Cys Thr Phe Ser Ala Thr Gly Cys Pro Ser Glu				
20	25	30		
caa cca aca tgc ctg tgg ttt cgc tac ggt gct cac cag cct gag aac				242
Gln Pro Thr Cys Leu Trp Phe Arg Tyr Gly Ala His Gln Pro Glu Asn				
35	40	45		
ctg tgc ttg gac ggg tgc aaa agt gag gca gas aag ttc aca gtg agg				290
Leu Cys Leu Asp Gly Cys Ser Glu Ala Xaa Lys Phe Thr Val Arg				
50	55	60		
gag gcc ctc aaa gaa aac caa gtt tcc ctc act gta aac aga gtg act				338
Glu Ala Leu Lys Glu Asn Gln Val Ser Leu Thr Val Asn Arg Val Thr				
65	70	75		
tca aat gac agt gca att tac atc tgc gga ata gca ttc ccc agt gtg				386
Ser Asn Asp Ser Ala Ile Tyr Ile Cys Gly Ile Ala Phe Pro Ser Val				
80	85	90	95	
ccg gaa gcg aga gct aaa cag aca gga gga ggg acc aca ctg gtg gta				434
Pro Glu Ala Arg Ala Lys Gln Thr Gly Gly Thr Thr Leu Val Val				
100	105	110		
aga gaa att aag ctg ctc agc aag gaa ctg cgg agc ttc ctg aca gct				482
Arg Glu Ile Lys Leu Leu Ser Lys Glu Leu Arg Ser Phe Leu Thr Ala				
115	120	125		
ctt gta tca ctg ctc tct gtc tat gtg acc ggt gtg tgc gtg gcc ttc				530
Leu Val Ser Leu Leu Ser Val Tyr Val Thr Gly Val Cys Val Ala Phe				
130	135	140		
ata ctc ctc tcc aaa tca aaa tcc aac cct cta aga aac aaa gaa ata				578
Ile Leu Leu Ser Lys Ser Lys Ser Asn Pro Leu Arg Asn Lys Glu Ile				
145	150	155		
aaa gaa gac tca caa aag aag agt gct cgg cgt att ttt cag gaa				626
Lys Glu Asp Ser Gln Lys Lys Ser Ala Arg Arg Ile Phe Gln Glu				
160	165	170	175	
att gct caa gaa cta tac cat aag aga cat gtg gaa aca aat cag caa				674
Ile Ala Gln Glu Leu Tyr His Lys Arg His Val Glu Thr Asn Gln Gln				
180	185	190		
tct gag aaa gat aac aac act tat gaa aac aga aga gta ctt tcc aac				722
Ser Glu Lys Asp Asn Asn Thr Tyr Glu Asn Arg Arg Val Leu Ser Asn				
195	200	205		
tat gaa agg cca tagaaacgtt ttaatttca atgaagtcac tgaaaatcca				774
Tyr Glu Arg Pro				
210				
actccaggag ctatggcagt gttaatgaac atatatcatc aggtctaaaa aaaaaataaa				834
ggttaactga aaagacaact ggctacaaag aaggatgcc aaatgttaagg aaactataac				894
taataktcat taccaaaata ctaaaaccca acaaaatgca actgaaaaat accttccaaa				954
tttgccaaaa aaaaaaw				971

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<222> 378..518

<221> sig\_peptide  
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score 5.5  
seq SLMTCTTINASA/IS

<221> polyA\_signal  
<222> 607..612

<221> polyA\_site  
<222> 628..640

<400> 257

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acggttcctg tcataatctt gggcttattt ggtgtgtgt tgaagggggg agactagaga	120
aatggcagg aacctttat ccggggcagg taggcgcctg tggactggg tgcctctggc	180
gtgcagaagc ttctctcttg gtgtgcctag attgatcgat ataaggctca ctctccccc	240
ccccaaatgt gttgatcgaa ggaacagaaaa aagggccatg ttcggagtgt atgacaacat	300
cgggatcctg ggaaactttt aaaagcaccc caaagaactg atcagggggc ccatatggct	360
tcgaggttgg aaaggaa atg aat tgc aac gtt gta tcc gaa aga gga aaa	410
Met Asn Cys Asn Val Val Ser Glu Arg Gly Lys	
-30 -25 -20	
tgg ttg gaa gta gaa tgt tcg ctg atg acc tgc aca acc tta ata aac	458
Trp Leu Val Glu Cys Ser Leu Met Thr Cys Thr Thr Leu Ile Asn	
-15 -10 -5	
gca tcc gct atc tct aca aac act tta acc gac atg gga agt ttc gat	506
Ala Ser Ala Ile Ser Thr Asn Thr Leu Thr Asp Met Gly Ser Phe Asp	
1 5 10	
aga aga gaa agc tgagaacttc ggaaaaggct catctgtcac cctggaraag	558
Arg Arg Glu Ser	
15	
ggaaactgtta cttttccctg tgagggaaacg gctttgtatt ttctctgtaa taaaatgggg	618
cttctttgga aaaaaaaaaaa aa	640

<210> 258  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 110..304

<221> sig\_peptide  
<222> 110..193  
<223> Von Heijne matrix  
score 4.59999990463257  
seq PLQWSLLVAVVAG/SV

<221> polyA\_signal  
<222> 708..713

<221> polyA\_site  
<222> 732..743

<400> 258

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gtctgtcccg ggtggacgac gccgtggctg ccaagcaccc ggcaccggc atg gcc ttt	118
Met Ala Phe	
ggc ttg cag atg ttc att cag agg aag ttt cca tac cct ttg cag tgg	166
Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro Leu Gln Trp	
-25 -20 -15 -10	
agc ctc cta gtg gcc gtg gtt gca ggc tct gtg gtc agc tac ggg gtg	214
Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser Tyr Gly Val	
-5 1 5	
acg aga gtg gag tcg gag aaa tgc aac aac ctc tgg ctc ttc ctg gag	262

Thr Arg Val Glu Ser Glu Lys Cys Asn Asn Leu Trp Leu Phe Leu Glu  
 10 15 20  
 acc gga cag ctc ccc aaa gac agg agc aca gat cag ara agc 304  
 Thr Gly Gln Leu Pro Lys Asp Arg Ser Thr Asp Gln Xaa Ser  
 25 30 35  
 taggagagct ccagcagggg cacagargat tgggggcagg argartctgg aacacakcct 364  
 tcatcccccc tgaccccagg ccgaccctcc ccacacccta gggtaaaaaa gtcgtatcct 424  
 ctgtcccgcat gtgtggccag gcctgacaaa cmccctgeaga tggctgtgc cccaaacctgg 484  
 gacctgcccc ggaggttggg gcagaaaaggg ctctccctgg ggtgggtttt ctcctcttagg 544  
 gtattggat gcatgttctg cactgccagc agagagggtg tgtctggggg ccaccaccta 604  
 tgggacacgg ggtcgaaggg gcctgtacac tctgtcattt ccttcttagc ccctgcacatct 664  
 ccaacaagtc caaggtgaca gctggtgcta gggcgtggg gttaataaat ggcttatcct 724  
 tctctccaaa araaaaaaaaam c 745

<210> 259  
 <211> 637  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> CDS  
 <222> 201..419  
  
 <221> sig\_peptide  
 <222> 201..272  
 <223> Von Heijne matrix  
 score 6.40000009536743  
 seq LSYLPLWLGPPIWP/CS  
  
 <221> polyA\_signal  
 <222> 601..606  
  
 <221> polyA\_site  
 <222> 627..637  
  
 <400> 259  
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 accccagaac ttggctccc ttcccttct ctctctggta gtcggagag ggctgtgatc 180  
 cagctccctg cctagcatcc atg acc tgt tgg atg tta cct cca atc agt ttc 233  
 Met Thr Cys Trp Met Leu Pro Pro Ile Ser Phe  
 -20 -15  
 ctg tcc tac ctg cct ctt tgg ctt gga cct ata tgg cca tgc tct ggc 281  
 Leu Ser Tyr Leu Pro Leu Trp Leu Gly Pro Ile Trp Pro Cys Ser Gly  
 -10 -5 1  
 tct acc ctt ggg aag cct gat ccc ggt gtg tgg ccc agc ttg ttc agg 329  
 Ser Thr Leu Gly Lys Pro Asp Pro Gly Val Trp Pro Ser Leu Phe Arg  
 5 10 15  
 ccc tgg gat gct gca tct cca ggc aac tat gca ctt tcc cgg gga rar 377  
 Pro Trp Asp Ala Ala Ser Pro Gly Asn Tyr Ala Leu Ser Arg Gly Xaa  
 20 25 30 35  
 aac cak tat gag aak tgg ggg cag ggc aca cat tca tct ttg 419  
 Asn Xaa Tyr Xaa Xaa Trp Gly Gln Gly Thr His Ser Ser Leu  
 40 45  
 targaaggta tggcctgggg tcrrggtaag gagggccag gtcagttctg gggtaact 479  
 gacccgtttt gccattctcc tggtggcgct gctgctccct gtttctggag ctggatgttc 539  
 cccacctggc agttgagctg cctgagccaa tggctgtc tttggtaact gagtgaacca 599  
 taataaaaggg gaacatggg ccctgtgaaa aaaaaaaaaa 637

<210> 260  
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 <212> DNA  
 <213> Homo sapiens  
  
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 <221> CDS  
 <222> 123..302  
  
 <221> sig\_peptide  
 <222> 123..176  
 <223> Von Heijne matrix  
 score 4.30000019073486  
 seq WTCLKSFPSPTSS/HA  
  
 <221> polyA\_signal  
 <222> 1279..1284  
  
 <221> polyA\_site  
 <222> 1301..1312  
  
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 aagagcatcc tgcgccccgg cgccccggcc tcaggcccct cccctggacc 60  
 cgccgcagag ccagtgcaga atacagaaaac tgccagccatg accacgcacg tcaccctggaa 120  
 ag atg ccc tgt cca acg tgg acc tgc ttg aag agc ttc ccc tcc ccg 167  
 Met Pro Cys Pro Thr Trp Thr Cys Leu Lys Ser Phe Pro Ser Pro  
     -15                  -10                  -5  
 acc agc agc cat gca tcg agc ctc cac ctt cct cca tca tgt acc agg 215  
 Thr Ser Ser His Ala Ser Ser Leu His Leu Pro Pro Ser Cys Thr Arg  
     1                  5                      10  
 cta act ttg aca caa act ttg agg aca gga atg cat ttg tca cgg gca 263  
 Leu Thr Leu Thr Gln Thr Leu Arg Thr Gly Met His Leu Ser Arg Ala  
     15                  20                  25  
 ttg caa ggt aca ttg acc agg cta cag tcc act cca gca tgaatgarat 312  
 Leu Gln Gly Thr Leu Thr Arg Leu Gln Ser Thr Pro Ala  
     30                  35                  40  
 gctggaggaa ggacatgakt atgcggtcat gctgtacacc tggcgagct gttcccggc 372  
 cattccccag gtgaaatgca acragcagcc caaccgakta raractatg araaraacagt 432  
 araggtgctg gagccggagg tcaccaagct catgaagttc atgtatccc arcgcaaggc 492  
 catcgagcgg ttctgcascg aggtgaagcg gctgtccat gccgagcgca ggaaggactt 552  
 tgtctctgag gcctacctcc tgacccttgg caagttcatac aacatgttg ctgtcctgg 612  
 tgagctaaag aacatgaast gcagcgtcaa raatgaccac tctgcctaca agagggcagc 672  
 acagttcctg cgaaagatgg cagatcccc cgttatccag gagtcgcaga acctttccat 732  
 gttcctggcc aaccacaaca ggtcaccca gtttctccac cagcaacttgg aagtgtatccc 792  
 aggctatgag gagctgctgg ctgacattgt caacatctgt gtggattact acgagaacaa 852  
 gatgtacctg actccccatg agaaacatata gtcctcaag gtaaaaactcc cctgaggccg 912  
 caccatgga gcctgggctt acccttcac cttcttctta taaaaaatcc gttttaaaaaa 972  
 acaatgttc tttttctta aacattgata cagatcttac ggcacataat gttttgttaac 1032  
 ctgttccttt cctgtaatat aatataccgt agtcacctt ccagatgtca ttaaggctat 1092  
 ttctacaatg ttatgtgtaa tgactgccaa gtattctgtt gtattggAAC attgtcatgt 1152  
 aacatataccc ctgtgggtgg atatttgcta aacttcattt aacacccttgg tagcagttt 1212  
 tgtgcacatc tttttgtcaa ggcaaaacttc cttagaagaga aattgctggc tcaaaggaa 1272  
 aaacagaata aatcgaaaaa tttatttcaa aaaaaaaaaa ccc 1315

<210> 261  
 <211> 1035  
 <212> DNA  
 <213> Homo sapiens

<220>  
<221> CDS  
<222> 98..673

<221> sig\_peptide  
<222> 98..376  
<223> Von Heijne matrix  
score 5.5999990463257  
seq VLLRQLFAQAEK/WY

<221> polyA\_site  
<222> 1025..1035

<400> 261  
aattttcygt ggtccaaacta ccctcgccga tcccaggctt ggcggggcac cgcctggcct 60  
ctccccgttcc tttaggctgc cgccgctgcc tgccgcc atg gca gag ttg ggc cta 115  
Met Ala Glu Leu Gly Leu  
-90  
aat gag cac cat caa aat gaa gtt att aat tat atg cgt ttt gct cgt 163  
Asn Glu His His Gln Asn Glu Val Ile Asn Tyr Met Arg Phe Ala Arg  
-85 -80 -75  
tca aag aga ggc ttg aga ctc aaa act gta gat tcc tgc ttc caa gac 211  
Ser Lys Arg Gly Leu Arg Leu Lys Thr Val Asp Ser Cys Phe Gln Asp  
-70 -65 -60  
ctc aag gag agc agg ctg gtg gag gac acc ttc acc ata gat gaa gtc 259  
Leu Lys Glu Ser Arg Leu Val Glu Asp Thr Phe Thr Ile Asp Glu Val  
-55 -50 -45 -40  
tct gaa gtc ctc aat gga tta caa gct gtg gtt cat agt gag gtg gaa 307  
Ser Glu Val Leu Asn Gly Leu Gln Ala Val Val His Ser Glu Val Glu  
-35 -30 -25  
tct gag ctc atc aac act gcc tat acc aat gtg tta ctt ctg cga cag 355  
Ser Glu Leu Ile Asn Thr Ala Tyr Thr Asn Val Leu Leu Arg Gln  
-20 -15 -10  
ctg ttt gca caa gct gag aag tgg tat ctt aag cta cag aca gac atc 403  
Leu Phe Ala Gln Ala Glu Lys Trp Tyr Leu Lys Leu Gln Thr Asp Ile  
-5 1 5  
tct gaa ctt gaa aac cga gaa tta tta gaa caa ktt gca gaa ttt gaa 451  
Ser Glu Leu Glu Asn Arg Glu Leu Leu Glu Gln Xaa Ala Glu Phe Glu  
10 15 20 25  
aaa gca rav att aca tct tca aac aaa aag ccc atc tta dat gtc aca 499  
Lys Ala Xaa Ile Thr Ser Ser Asn Lys Lys Pro Ile Leu Xaa Val Thr  
30 35 40  
aas cca aaa ctt gct cca ctt aat gaa ggt gga aca gca aaa ctc cta 547  
Xaa Pro Lys Leu Ala Pro Leu Asn Glu Gly Thr Ala Lys Leu Leu  
45 50 55  
aac aag gta ata tgt att att ttg aga aac gga aag tct ctc att ctg 595  
Asn Lys Val Ile Cys Ile Ile Leu Arg Asn Gly Lys Ser Leu Ile Leu  
60 65 70  
tcc tgt cat tgc cta ggg tgg aga aac aaa agt gga agg ttt gtt tca 643  
Ser Cys His Cys Leu Gly Trp Arg Asn Lys Ser Gly Arg Phe Val Ser  
75 80 85  
ggc cct ctg agg ata att agt cca ttg cag tagtttact tgatggtacc 693  
Gly Pro Leu Arg Ile Ile Ser Pro Leu Gln  
90 95  
ccatggcca gaagaggcga tacttaacct tctagagagc ctgaagttagc tcctgatcac 753  
acctttcaa ggtaaagtga agagcatgaa attttggaca gcgttatttg atggacattt 813  
aaagtttgtg atctgcgtta acaaggagaa gggttttaa gttataaaa attatttatac 873  
aattagccgg gtgtgggtt acgtgcctat agtcagagct actcgggagg ctgaggcagg 933  
agaattgcctt gaacccggga ggtggaggtt gcagtgcgt gagatcacgc cactgcactc 993  
tagcctggc gacagagcga gactccatct caaaaaaaaaaa aa 1035

<210> 262  
 <211> 696  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 17..463

<221> sig\_peptide  
 <222> 17..232  
 <223> Von Heijne matrix  
 score 3.79999995231628  
 seq LMGLALAVYKCQS/MG

<221> polyA\_signal  
 <222> 657..662

<221> polyA\_site  
 <222> 684..696

<400> 262

actcaaacag attccc atg aat ctc ttc atc atg tac atg gca ggc aat act	52		
Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr			
-70	-65		
atc tcc atc ttc cct act atg atg gtg tgt atg atg gcc tgg cga ccc	100		
Ile Ser Ile Phe Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro			
-60	-55	-50	-45
att cag gca ctt atg gcc att tca gcc act ttc aag atg tta gaa agt	148		
Ile Gln Ala Leu Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser			
-40	-35	-30	
tca agc cag aag ttt ctt cag ggt ttg gtc tat ctc att ggg aac ctg	196		
Ser Ser Gln Lys Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu			
-25	-20	-15	
atg ggt ttg gca ttg gct gtt tac aag tgc cag tcc atg gga ctg tta	244		
Met Gly Leu Ala Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu			
-10	-5	1	
cct aca cat gca tcg gat tgg tta gcc ttc att gag ccc cct gag aga	292		
Pro Thr His Ala Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg			
5	10	15	20
atg gag tca gtg gtg gag gac tgc ttt tgt gaa cat gag aaa gca gcg	340		
Met Glu Ser Val Val Glu Asp Cys Phe Cys Glu His Glu Lys Ala Ala			
25	30	35	
cct ggt ccc tat gta ttt ggg tct tat tta cat cct tct tta agc cca	388		
Pro Gly Pro Tyr Val Phe Gly Ser Tyr Leu His Pro Ser Leu Ser Pro			
40	45	50	
gtg gct cct cag cat act ctt aaa cta atc act tat gtt aaa aaa aac	436		
Val Ala Pro Gln His Thr Leu Lys Leu Ile Thr Tyr Val Lys Lys Asn			
55	60	65	
caa aaa act ctt ttc tcc atg gtg ggg tgacaggtcc taaaaggaca	483		
Gln Lys Thr Leu Phe Ser Met Val Gly			
70	75		
atgtgcatac tacgacaaac acaaaaaaaaac tataccataa cccagggtcg aaaataatgt	543		
aaaaaaaaacttt atttttgttt ccagtacaga gcaaaaaaac aaaaaaaaaa cataactatg	603		
taaacaaaaa aataactgct gctaaatcaa aaactgttgc agcatctcct ttcaataaat	663		
taaatggtg araacaatgc aaaaaaaaaaaa aaa	696		

<210> 263  
 <211> 868

<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 263..481

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<221> sig_peptide
<222> 263..322
<223> Von Heijne matrix
      score 11.1999998092651
      seq ILVVLMLGLPLAQA/LD
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<221> polyA\_site  
<222> 858..868

<210> 264  
<211> 775  
<212> DNA  
<213> *Homo sapiens*

<220>  
<221> CDS  
<222> 42..299

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<221> sig_peptide
<222> 42..101
<223> Von Heijne matrix
      score 5.40000009536743
      seq WFWHSSALGLVLA/PP
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<221> polyA\_site

&lt;222&gt; 762..775

&lt;400&gt; 264

aacgatacaa atggtaggcc ttcatgtgag ccagtdacta c atg aat ctt cat ttc	56
Met Asn Leu His Phe	
-20	
cca cag tgg ttt gtt cat tca tca gcg tta ggc ttg gtc ctg gct cca	104
Pro Gln Trp Phe Val His Ser Ser Ala Leu Gly Leu Val Leu Ala Pro	
-15 -10 -5 1	
cct ttc tcc tct ccg ggc act gac ccc acc ttt ccg tgt att tac tgt	152
Pro Phe Ser Ser Pro Gly Thr Asp Pro Thr Phe Pro Cys Ile Tyr Cys	
5 10 15	
agg cta tta aat atg atc atg acc cgc ctt gca ttt tca ttc atc acc	200
Arg Leu Leu Asn Met Ile Met Thr Arg Leu Ala Phe Ser Phe Ile Thr	
20 25 30	
tgt tta tgc cca aat tta aag gaa gtt tgt ctc att ttg cca gaa aaa	248
Cys Leu Cys Pro Asn Leu Lys Glu Val Cys Leu Ile Leu Pro Glu Lys	
35 40 45	
aat tgt aat agt cga cac gct gga ttt gta ggg cca sca aaa ttg cg	296
Asn Cys Asn Ser Arg His Ala Gly Phe Val Gly Pro Xaa Lys Leu Arg	
50 55 60 65	
cag tgaaaactwkk ttcwttctca aagcccttca ttccccacaa ggttaagctc	349
Gln	
tcgaaacccc atttgatcct tggttcctat ttcatcctc ctttggaaatc tgaaaatcg	409
tctccatgtt gtatgcaa at taakttgc ctgtttgtt actcttccaa cacagggtat	469
cagggaraaa gaggccttat ctgttccctcc atccccctg ttttgacaga ctgctaagaa	529
ttccttcagga cttcccttgg ttgggattt tactttccca aaagtctgat ctgatttctt	589
tcagggtag acaagcttgt cctagtctc tgcttcaggt cttatcagaa gaaacccagg	649
aatagaaaaag gtagatgcct tgactttgt ccctgttgc gggactaaag tgtttttgc	709
cagaattgtc aaaagctccg gttcaaactc tgtagagttt catggaaaaa caaaacaaaa	769
aaaaaa	775

&lt;210&gt; 265

&lt;211&gt; 1075

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 198..431

&lt;221&gt; sig\_peptide

&lt;222&gt; 198..260

&lt;223&gt; Von Heijne matrix

score 6.90000009536743

seq LLACGSLLPGLWQ/HL

&lt;221&gt; polyA\_site

&lt;222&gt; 1064..1074

&lt;400&gt; 265

atatatttct gaggcagtac ccatctcaact tgtaaactta aaagacacccg cagagatttg	60
agggactcag aagtcaaata gagtaggtt aaaaacctttt attttcaaa ttaattgttt	120
taagaaacaa gcatacctgt gtaagtgaaa tatcttaatt tttgtgttaat caagtttagga	180
gacagagatt ctcatga atg tgt cct gtg ttc tca aag cag ctg cta gcc	230
Met Cys Pro Val Phe Ser Lys Gln Leu Leu Ala	
-20 -15	
tgt ggg tct ctc cta cct ggg tta tgg cag cac ctc aca gcc aat cac	278
Cys Gly Ser Leu Leu Pro Gly Leu Trp Gln His Leu Thr Ala Asn His	
-10 -5 1 5	

tgg cct cca ttc tcc sct ttc ctc tgt aca gtt tgc tct ggt tcc tca	326
Trp Pro Pro Phe Ser Xaa Phe Leu Cys Thr Val Cys Ser Gly Ser Ser	
10 15 20	
gag cag att tcc gag tat act gct tca gcc acg ccc cca ctg tgc cgt	374
Glu Gln Ile Ser Glu Tyr Thr Ala Ser Ala Thr Pro Pro Leu Cys Arg	
25 30 35	
tcc ctg aac caa gag cca ttc gty tca aga gcc att cgt cca aag tac	422
Ser Leu Asn Gln Glu Pro Phe Val Ser Arg Ala Ile Arg Pro Lys Tyr	
40 45 50	
tct atc acc tagccattgt akccatacca agccgggctt cctactttccc	471
Ser Ile Thr	
55	
tctgctcccc ttggtttcct cctgtraart aaatctcaact gacccttgat gcasctccaa	531
gcatatataa tatatatata ataaaaccat abtctaaaaaa attcaaaccat ggawaaataa	591
asccaraaat ttgtatggga aaaatctgca caaatttatt tggccagcat ggttatcatg	651
gctctattga atttattcctt gaccgtcttt aaagccaaag caaacgggat aaagtgtatca	711
actacttacc tctcaataacc aaaaargaag caggaggcaa aatctctcaw taatttcata	771
aaaacaattc ttakctgggc gcggtggtc wcacctgtar tcccaacact ttgggaggcc	831
saggtggcg gatcatgagg tcgggagatc aamaccatcc tggctaacat ggtgaaaccc	891
catctctact aaaattacaa aaaattrgct gggcgagggt gcgggcacct gtggtccccag	951
ctactcggga ggctgaggca agagaatggt gtgaacccca gggggcggag cctgcagtga	1011
gctgagatcg caccactgca ctccagcctg ggcgacagtg agactccgtc taaaaaaaaa	1071
aaah	1075

<210> 266  
<211> 981  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 279..473

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<221> sig_peptide
<222> 279..362
<223> Von Heijne matrix
      score 4.4000009536743
      seq SCFLVALIIWCYL/RE
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<221> polyA\_signal  
<222> 944..949

<221> polyA\_site  
<222> 970..981

<400> 266  
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 gggcagacac cggcgccgg gcggasgctt actgctctt ctcttccagg gccgtccggg 120  
 cgctgaggct cataggctgg gcttccgaa gccttcatcc gttccccgtt tcccgggatc 180  
 gggcccaccc tgccgcgcag gaagaggacg accctgaccg cccatttagat ttttcctcca 240  
 gcaaagccaa ccctcacccgc tggtcgggtgg gccataacc atg gga aag gga cat cag 296  
 Met Gly Lys Gly His Gln  
 -25.

cg <sup>g</sup> cc <sup>c</sup> tgg tgg aag gt <sup>g</sup> ct <sup>g</sup> ccc ctc agc tgc ttc ctc gt <sup>g</sup> gc <sup>g</sup> ct <sup>g</sup>	344		
Arg Pro Trp Trp Lys Val Leu Pro Leu Ser Cys Phe Leu Val Ala Leu			
-20	-15	-10	
atc atc tgg tgc tac ct <sup>g</sup> agg gag gag agc gag gc <sup>g</sup> gac cag tgg tt <sup>g</sup>	392		
Ile Ile Trp Cys Tyr Leu Arg Glu Glu Ser Glu Ala Asp Gln Trp Leu			
-5	1	5	10
aga cag gt <sup>g</sup> tgg gga gag gt <sup>g</sup> cca gag ccc agt gat cgt tct gag gag	440		

Arg Gln Val Trp Gly Glu Val Pro Glu Pro Ser Asp Arg Ser Glu Glu			
15	20	25	
cct gag act cca gct gcc tac aga gcg aga act tgacgggtg cccgctgggg	493		
Pro Glu Thr Pro Ala Ala Tyr Arg Ala Arg Thr			
30	35		
ctggcaggaa gggagccgac asccgcctt cggatttgat ktcacgtttg cccgtgactg	553		
tcctggctat gcktgcgtcc tcagcaactra argacttggc tggatgg ggcacttggc	613		
tatgctgatt cgctgaagg cggavcaaaa ttcagcaaa tcggaaactg ctcctcsct	673		
ggcttgcatt ktccaaggat tccatccgca aaacttctca ratccttggg gaaggttca	733		
gttgcactgt atgctgttgg atttgccaag tctttgtata acataatcat gtttccaaag	793		
cacttcttgtt gacacttgc atccagttt agtttgcagg taatttgctt tctgagatag	853		
aatatctggc agaagtgtga aactgtattt catgctgcgg cctgtcaag gaacacttcc	913		
acatgtgagt ttacacaac aacaaatgaa aataaaatttt aattttataa tatggaaaaa	973		
aaaaaaaaaa	981		

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<222> 1002..1007	
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acacccaagga g atg ctc ctt agt att aca act gct tat aca ggt ctg	50
Met Leu Leu Leu Ser Ile Thr Thr Ala Tyr Thr Gly Leu	
-25 -20 -15	
gaa tta act ttc ttc tct ggt gta tat gga acc tgt att ggt gct aca	98
Glu Leu Thr Phe Phe Ser Gly Val Tyr Gly Thr Cys Ile Gly Ala Thr	
-10 -5 1	
aat aaa ttt gga gca gaa gag ara agc ctt att gga ctt tct ggc att	146
Asn Lys Phe Gly Ala Glu Glu Xaa Ser Leu Ile Gly Leu Ser Gly Ile	
5 10 15	
ttc atc ggc att gga gaa att tta ggt gga agc ctc ttc ggc ctg ctg	194
Phe Ile Gly Ile Gly Glu Ile Leu Gly Ser Leu Phe Gly Leu Leu	
20 25 30	
agc aag aac aat cgt ttt ggt aga aat cca gtt gtg ctg ttg ggc atc	242
Ser Lys Asn Asn Arg Phe Gly Arg Asn Pro Val Val Leu Leu Gly Ile	
35 40 45 50	
ctg gtg cac ttc ata gct ttt tat cta ata ttt ctc aac atg cct gga	290
Leu Val His Phe Ile Ala Phe Tyr Leu Ile Phe Leu Asn Met Pro Gly	
55 60 65	
gat gcc ccg att gct cct gtt aaa gga act gac agc agt gct tac atc	338
Asp Ala Pro Ile Ala Pro Val Lys Gly Thr Asp Ser Ser Ala Tyr Ile	
70 75 80	
aaa tcc agc aaa raa ttt gcc att ctc tgc akt ttt ctg tkg ggc ctt	386
Lys Ser Ser Lys Xaa Phe Ala Ile Leu Cys Xaa Phe Leu Xaa Gly Leu	

85	90	95	
gga aac agc tgc ttt aat acc cas ctg ctt akt atc tkg ggc ttt ctg			434
Gly Asn Ser Cys Phe Asn Thr Xaa Leu Leu Xaa Ile Xaa Gly Phe Leu			
100	105	110	
tat tct gaa rac agc gcc cca kca ttt gcc atc ttc aat ttt gtt cag			482
Tyr Ser Glu Xaa Ser Ala Pro Xaa Phe Ala Ile Phe Asn Phe Val Gln			
115	120	125	130
tct att tgc gca gcc gtg gca ttt ttc tac agc aac tac ctt ctc ctt			530
Ser Ile Cys Ala Ala Val Ala Phe Phe Tyr Ser Asn Tyr Leu Leu			
135	140	145	
cac tgg caa ctc ctg gtc atg gtk atw ttt ggg ttt ttk gga aca att			578
His Trp Gln Leu Leu Val Met Val Ile Phe Gly Phe Xaa Gly Thr Ile			
150	155	160	
tct ttc ttc act gtg gaa tgg gaa sct gcc gcc ttt gta scc cgc ggc			626
Ser Phe Phe Thr Val Glu Trp Glu Xaa Ala Ala Phe Val Xaa Arg Gly			
165	170	175	
tct gac tac cga agt atc tgatctggtg tccgtgaggg gacacgtatg			674
Ser Asp Tyr Arg Ser Ile			
180			
accccgaaaa cacagctgga cacagagctt ggtggaagaaa gtcgcctttg atcttcacta			734
tatattgggt gatgttcagt atggaaaatc aagggtttaaa gactgttaaa tcagccagag			
tkgggtgtca agtttacaga tatgagttat ttaaagcaag tagaataagg gaaagctgtt			
ctgtcaactg taattgttca aagatgttgt ttgcatttc atctatctca attcttataa			
tcatgttata gaatgtaaat gtttcttct ctctcctgct cttgttggaa gatcctgcct			
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score 7.69999980926514			
seq LVLFLSLALLVTP/TS			
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Met Ser Thr Trp Tyr Leu Ala Leu			
-80	-75		
aat aag tcc tat aag aat aaa gac agc gtt agg att tat ctc agc ttg			
Asn Lys Ser Tyr Lys Asn Lys Asp Ser Val Arg Ile Tyr Leu Ser Leu			
-70	-65	-60	
tgc aca gtg agc att aaa ttg aca tac ttt cat gat ata cag act aat			
Cys Thr Val Ser Ile Lys Phe Thr Tyr Phe His Asp Ile Gln Thr Asn			
-55	-50	-45	
tgt ctt aca aca tgg aaa cat tcg aga tgc aga ttt tat tgg gca ttt			
Cys Leu Thr Thr Trp Lys His Ser Arg Cys Arg Phe Tyr Trp Ala Phe			
-40	-35	-30	-25
ggt ggt tcc att tta cag cac tca gtg gat ccc ctt gtt ttg ttc cta			
Gly Gly Ser Ile Leu Gln His Ser Val Asp Pro Leu Val Phe Leu			
306			

-20	-15	-10	
agc ctg gcc ctg tta gtg aca ccc act tcc acc cct tct gct aar ata			354.
Ser Leu Ala Leu Leu Val Thr Pro Thr Ser Thr Pro Ser Ala Lys Ile			
-5	1	5	
car agc ctt caa att gac ctc cct gga ggc tgg agg ctg gcc act gac			402
Gln Ser Leu Gln Ile Asp Leu Pro Gly Gly Trp Arg Leu Ala Thr Asp			
10	15	20	
agg atc ttt acc ctc tcc ccc gta ccc atg gac rgc ccc ctc atc ctt			450
Arg Ile Phe Thr Leu Ser Pro Val Pro Met Asp Xaa Pro Leu Ile Leu			
25	30	35	40
cat cag ttg taaaggtaga tatttgttcc ttggagtcca acatcatgct			499
His Gln Leu			
gttcagaata taatgagatc aatagttgaa aaactagata tacatgccac ccwgacaaag			559
ctattaagtt attaagtgtc agccctggat cttggcttat tgtgaaatgt taattatttt			619
atcactcyat taagaagctg tgggctccat ctcagcattg aaaagggact aatttgcct			679
gttttggaat tgaatttagct ttcagccas cagggcactg tttgttaat tgcttttcc			739
agtacttagca tggggctcc tcctccatagcc tctgttagct tctgagcttg taacctccag			799
ggaaaavatga gaatattcac ccttttaata tttgttagaga ccatgcaga ccattgtctt			859
ctaataatta gaaataactta gcccaggattct ctatagtaaa cccggagatt gggagggctg			919
ctttctactt ggtgcaccc tctgcgttcc taatgatttt taaaaatctg ttaataattt			979
atgttttctg gctgggcaca gttggctcacg cctgttaatcc cagcactttg ggaggccaag			1039
gagggcgagat catgaggtca ggagattgar accatcctgg ctaaacacggt gaaaccccg			1099
ctctactaaa aatacaaaaar aattakccgg gcatggtagt gggccctgt gtacccagct			1159
actggggagg ctgaggcarg araaatcgctt gaacctggga ggcggagggtt gcastragct			1219
gagatggtgc caccgcactc tagcctgggt gacagagcga gacttcattt caaaaaaaaaa			1279
aamc			1283

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<222> 70..327

<221> sig\_peptide  
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score 9.60000038146973  
seq WLIALASWSWALC/RI

<221> polyA\_signal  
<222> 1741..1746

<221> polyA\_site  
<222> 1763..1774

<400> 269  
agccccgttt cgtgccccgca gccgactgca casctgtccg cgagctctgag atacttacag  
agagctaca atg gaa aag tcc tgg atg ctg tgg aac ttt gtt gaa aga tgg  
Met Glu Lys Ser Trp Met Leu Trp Asn Phe Val Glu Arg Trp  
-25 -20 -15  
cta ata gcc ttg gct tca tgg tct tgg gct ctc tgc cgt att tct ctt  
Leu Ile Ala Leu Ala Ser Trp Ser Trp Ala Leu Cys Arg Ile Ser Leu  
-10 -5 1  
tta cct tta ata gtg act ttt cat ctg tat gga ggc att atc tta ctt  
Leu Pro Leu Ile Val Thr Phe His Leu Tyr Gly Gly Ile Ile Leu Leu  
5 10 15 20  
ttg tta ata ttc ata tca atw kca ggt att ctg tat aaa ttc cas gat  
255

<210> 270  
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<212> DNA  
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<220>  
<221> CDS  
<222> 12..497

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<222> 12..104
<223> Von Heijne matrix
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      seq LVGVLFVSVTTG/PW
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<221> polyA\_signal  
<222> 935..940

<221> polyA\_site  
<222> 955..967

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      Met Ala Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu
      -30          -25          -20
gcc gtg acg gcc aga ctc gtt ggt gtc ctg tgg ttc gtc tca gtc act 98
      Ala Val Thr Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr

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-15	-10	-5	
aca gga ccc tgg ggg gct gtt gcc acc tcc gcc ggg ggc gag gag tcg			146
Thr Gly Pro Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser			
1	5	10	
ctt aag tgc gag gac ctc aaa gtg gga caa tat att tgt aaa gat cca			194
Leu Lys Cys Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro			
15	20	25	30
aaa ata aat gac gct acg caa gaa cca gtt aac tgt aca aac tac aca			242
Lys Ile Asn Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr			
35	40	45	
gct cat gtt tcc tgt ttt cca gca ccc aac ata act tgt aag gat tcc			290
Ala His Val Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser			
50	55	60	
agt ggc aat gaa aca cat ttt act ggg aac gaa gtt ggt ttt ttc aag			338
Ser Gly Asn Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys			
65	70	75	
ccc ata tct tgc cga aat gta aat ggc tat tcc tac aat gag cag tcg			386
Pro Ile Ser Cys Arg Asn Val Asn Gly Tyr Ser Tyr Asn Glu Gln Ser			
80	85	90	
cat gtc tct ttt tct tgg atg gtt ggg agc aga tcg att tta cct tgg			434
His Val Ser Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp			
95	100	105	110
ata ccc tgc ttt ggg ttt gtt aaa btt tyg cac tgt agg gtt tkg tgg			482
Ile Pro Cys Phe Gly Phe Val Lys Xaa Xaa His Cys Arg Val Xaa Trp			
115	120	125	
aat tgg gag cct aat tgatttcaty cttatccaa tgcagattgt tggaccttca			537
Asn Trp Glu Pro Asn			
130			
aatggaagta gttacattat agattactat ggaaccagac ttacaagact gagtattact			597
aatgaaacat ttagaaaaac gcaattatat ccataaatat ttttaaaag aaacagattt			657
gaggcctcctt gatTTAATA gagaacttct agtgtatggat ttaaagatt tctcttttc			717
attcatatac cattttatga gttctgtata atttttgc gttttgttt ttttgagat			777
aagtatatta ttgtgagatt tatttaatag gacttcctt gaaagctgta taatagtgtt			837
tctcgccctt ctgtctctat gagagatagc ttattactt gataactctt aatctttac			897
aaaggcaagt tgccacttgt cattttgtt tctgaaaaat aaaagtataa cttattcaca			957
aaaaaaaaaaa mms			970

<210> 271  
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<212> DNA  
<213> Homo sapiens

<220>  
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<222> 90..383

<221> sig\_peptide  
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<223> Von Heijne matrix  
score 4.90000009536743  
seq MLIMLGIFFNVHS/AV

<221> polyA\_signal  
<222> 609..614

<221> polyA\_site  
<222> 632..643

<400> 271  
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cacctcggcg atccccgact cccttcttt atg gcg tcg ctc ctg tgc tgt ggg Met Ala Ser Leu Leu Cys Cys Gly -35 -30 -35 -30	113
ccg aag ctg gcc tgc ggc atc gtc ctc agc gcc tgg gga gtg atc Pro Lys Leu Ala Ala Cys Gly Ile Val Leu Ser Ala Trp Gly Val Ile -25 -20 -25 -20 -15	161
atg ttg ata atg ctc gga ata ttt ttc aat gtc cat tcc gct gtg ttg Met Leu Ile Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu -10 -5 1	209
att gag gac gtt ccc ttc acg gag aaa gat ttt gag aac ggc ccc car Ile Glu Asp Val Pro Phe Thr Glu Lys Asp Phe Glu Asn Gly Pro Gln 5 10 15	257
aac ata tac aac ctt tac rag caa ktc agc tac aac tgt ttc atc gct Asn Ile Tyr Asn Leu Tyr Xaa Gln Xaa Ser Tyr Asn Cys Phe Ile Ala 20 25 30 35	305
gca ggc ctt tac ctc ctc gga ggc ttc tct ttc tgc caa ktt cgg Ala Gly Leu Tyr Leu Leu Gly Phe Ser Phe Cys Gln Xaa Arg 40 45 50	353
ctc aat aag cgc aag gaa tac atg gtg cgc tagggccccc gcgcgtttcc Leu Asn Lys Arg Lys Glu Tyr Met Val Arg 55 60	403
ccgctccagc ccctcctcta tttaaaract ccctgcaccg tktcacccag gtcgcgtccc acccttgccg gcgcctctg tggactggg tttccggc rararactga atcccttctc ccatctctgg catccggccc ccgtggarar ggctgaggct gggggctgt tccgtctctc cacccttcgc tgtgtcccgat atctcaataa agagaatctg ctctttcaa aaaaaaaaaa my	463 523 583 643 645

<210> 272  
<211> 773  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 332..541

<221> sig\_peptide  
<222> 332..376  
<223> Von Heijne matrix  
score 3.59999990463257  
seq FLPCCLLWSVFNP/ES

<221> polyA\_signal  
<222> 739..744

<221> polyA\_site  
<222> 761..773

<400> 272  
aaaacaattc atgccttca tagtttatta ttattaaagt ctaaacaaaa ttgcaatttc  
ttagtaacc ttatattac aataaatgaa gattaccctc aaatgttaga agctgtctag  
gtccgtccgg tgtgtcagat tttcctcaga ttagatgtgc caataaccaa gtttattcag  
taaacaacct gtactgttt catctggttt tattactctc acccataaac agtaatgact  
ctctgaccct ctggaaatat gtaatgcttc caatcttgct ttgtgtatct catttaattt  
gttataaggt agtactgatt ttagcatatt a atg cga ttt ctt cct tgt tgt  
Met Arg Phe Leu Pro Cys Cys  
-15 -10 -15 -10

ttg ctt tgg tct gtg ttc aat cca gag agc tta aat tgt cat tat ttt Leu Leu Trp Ser Val Phe Asn Pro Glu Ser Leu Asn Cys His Tyr Phe -5 1 5	400
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ghk ndd gaa amc tgt att ttt gyt agt tta caa tat tat gaa att tca	448
Xaa Xaa Glu Xaa Cys Ile Phe Xaa Ser Leu Gln Tyr Tyr Glu Ile Ser	
10 15 20	
ctt cag gag aaa ctg ctg ggc ttc ctg tgg ctt tgt ttt ctt agt tac	496
Leu Gln Glu Lys Leu Leu Gly Phe Leu Trp Leu Cys Phe Leu Ser Tyr	
25 30 35 40	
ttt ttc cgt gcc gtg tat ttt tta att gat ttt tct tct ttt act	541
Phe Phe Arg Ala Val Tyr Phe Leu Ile Asp Phe Ser Ser Phe Thr	
45 50 55	
tggaaaagaaaa gtgttttatt ttccaaatctg gtccatattt acattcttagt tcagagccaa	601
gcctttaact gtacagaatt tccactgtaa taaaaactat tttagtgttag ttataaatag	661
ccttcaaaaaa gagagattct ccattacacg atcacctgca tcacagccca tggtgaatgt	721
atgtttctgc atagcgaaaat aaaaatggca aatgcactga aaaaaaaaaaa aa	773

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<210> 273  
<211> 566  
<212> DNA  
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 43..222

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<222> 43..177
<223> Von Heijne matrix
      score 4
      seq ENFLSLLSKSCSA/DP
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<221> polyA\_signal  
<222> 530..535

<221> polyA\_site  
<222> 555..566

<400> 273

aacgagtgga ggtgtggcta gtggctgtga tgagataaat cc atg cat agc ctt  
Met His Ser Leu  
-45

ttc att gcg agc ttg aaa gtt ctt ttc tat tac agt ttt agc ttt agg 102  
Phe Ile Ala Ser Leu Lys Val Leu Phe Tyr Tyr Ser Phe Ser Phe Arg  
-40 -35 -30

ttt aat tgg ttc gac tgc ctt ctc cac aat ttg ggc gag aat ttc ctt 150  
Phe Asn Trp Phe Asp Cys Leu Leu His Asn Leu Gly Glu Asn Phe Leu  
-25 -20 -15 -10

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      -20          -15          -10
agc ctt ctc agc aaa agt tgt tct gct gac ccg tct ggg tca act ttc 198
Ser Leu Leu Ser Lys Ser Cys Ser Ala Asp Pro Ser Gly Ser Thr Phe
      -5           1           5

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-3 1 5  
atg agg gac att gag aca aac aaa tgaaatatgg gttaaagtac tctgagcagc 252  
Met Arg Asp Ile Glu Thr Asn Lys  
10 15

10	15	
tacaaaaaaga araccagtct atcctgctgg agacagtggc cacgtgaara aagagcttt		312
gcagtatgaa agaccacatg gaaagagagg ccacatggaa ccaacagtca gcatcttgg		372
ttcggacacg tgaaraaaatt catctcarac tgtgtatcct aaatcaggca cttgctgaat		432
ctaactacat gagtgagacc agttgacaac acatggagca racatgagct gttctcagt		492
artcctacac aaattcctga ctcacaacac tgtgagcaat aaaatggttg ttatTTtaag		552
ccaaaaaaaaaaaa	aaaa	566

<210> 274  
<211> 455  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 115..231

<221> sig\_peptide  
<222> 115..180  
<223> Von Heijne matrix  
score 5  
seq HLFVTWSSQRALS/HP

<221> polyA\_signal  
<222> 419..424

<221> polyA\_site  
<222> 445..455

<400> 274  
aacctgccag tkatgcaa at gccaaaatgt gggtcatcat atatgtatatt tgaaaccttt 60  
ctgaacatgt acaccaccca atgcttagagg ctgacttgga aaccgggtggg tgca atg 117  
Met  
ccc gag gct gtg gaa caa tca gcc cat ctc ttt gtg acc tgg agc agt 165  
Pro Glu Ala Val Glu Gln Ser Ala His Leu Phe Val Thr Trp Ser Ser  
-20 -15 -10  
cag agg gcc ctc agt cac ccc gcc cca ttc ctc acc ara raa aar aat 213  
Gln Arg Ala Leu Ser His Pro Ala Pro Phe Leu Thr Xaa Xaa Lys Asn  
-5 1 5 10  
cca ttt cta tgg aag ctc tgacgttaact tcagtgtttt ctacaataact 261  
Pro Phe Leu Trp Lys Leu  
15  
cctcctgccc cggccccatta aaacagttct tttgttaaaa aatavcctaa tggtccaaact 321  
ttgctgtctg ttcttccaaa tgtttataat acacattatt tataaatatg tctgtttggg 381  
aagctaagaa caagctagtt tttacaacac aaatggaaat aaatgcaatt attataaaaaa 441  
tyaaaaaaaaaaaa 455

<210> 275  
<211> 673  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 232..384

<221> sig\_peptide  
<222> 232..300  
<223> Von Heijne matrix  
score 3.70000004768372  
seq FFLCAAFPLGAGV/KM

<221> polyA\_signal  
<222> 650..655

<221> polyA\_site  
<222> 662..673

<400> 275

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agccttagtt	tccccatggcc	ctgaaacaca	cacatttccc	ccttccttcc	ccagaagcca	180
ctggccccc	atagcaccca	gtgcacccctt	tttacaagtg	gaagaactag	g atg gct	237
					Met Ala	
ttc caa agt ctt cta gaa atg aag ttc ttt ctc tgt gca gct ttc ccc						285
Phe Gln Ser Leu Leu Glu Met Lys Phe Phe Leu Cys Ala Ala Phe Pro						
-20	-15	-10				
ctt gga gca gga gtg aag atg ttt cat tat ctt ggg cct ggg aaa cca						333
Leu Gly Ala Gly Val Lys Met Phe His Tyr Leu Gly Pro Gly Lys Pro.						
-5	1	5	10			
ctt cyy cag gct tct ccc tcc ccc cac ccc cat agg amc agg att tgg						381
Leu Xaa Gln Ala Ser Pro Ser Pro His Pro His Arg Xaa Arg Ile Trp						
15	20	25				
cct tagttctgg gcctatcsgc tgccctccct cttyttccta ccacctcttc						434
Pro						
tgccttcctt trawctctgt tgggcttggg gatcttagtt ttctttgtt tatttcccat						494
ctcattttt tcttctggc agttttta agggggggtg ttgtggtttt ttgttttgt						554
tttgcctctg aaaaarcatt tgcccttcctt cctctcccaa cataacaatc gtggtaacag						614
aatgcgactg ctgatttacc gatgtattta atgtaagtaa aaaaaggaaa aaaaraaaa						673

&lt;210&gt; 276

&lt;211&gt; 639

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 143..427

&lt;221&gt; sig\_peptide

&lt;222&gt; 143..286

&lt;223&gt; Von Heijne matrix

score 7.5

seq FVILLFIFTVVVS/LV

&lt;221&gt; polyA\_signal

&lt;222&gt; 606..611

&lt;221&gt; polyA\_site

&lt;222&gt; 628..639

&lt;400&gt; 276

aatcgcttca	gcagcatcct	ctcagacaag	agccactatt	tctgattcag	atcacctgtc	60	
atcgaagttt	aaagaagggg	aaacaggaga	cagaaataca	ctgaacccaa	aagattcaa	120	
agagcaagtg	gaatctctaa	ga atg	gct tcc	agc cac	tgg aat	gaa acc act	172
					Met Ala	Ser Ser His Trp Asn Glu Thr Thr	
				-45	-40		

acc tct gtt tat	cag tac ctt	ggt ttt	caa gtt	caa aaa	att tac cct	220
Thr Ser Val	Tyr Gln Tyr	Leu Gly	Phe Gln Val	Gln Lys	Ile Tyr Pro	
-35	-30	-25				

ttc cat gac aac	tgg aac act	gcc tgc	ttt gtc	atc ctg	ctt tta	ttt	268
Phe His Asp	Asn Trp	Asn Thr	Ala Cys	Phe Val	Ile Leu	Leu Phe	
-20	-15	-10					

ata ttt aca	gtg gta	tct tta	gtg gtg	ctg gct	ttc ctt	tat gaa	gtg	316
Ile Phe Thr	Val Val	Ser Leu	Val Val	Leu Ala	Phe Leu	Tyr Glu	Val	
-5	1	5	10					

ctt gam wgc	tgc tgc	tgt gta	aaa aac	aaa acc	gtg aaa	gac ttg	aaa	364
Leu Xaa Cys	Cys Cys	Val Lys	Asn Lys	Thr Val	Lys Asp	Leu Lys		

15	20	25	
agt gaa ccc aac cct ctt ara akt atg atg gac aac atc aga aaa cgt			412
Ser Glu Pro Asn Pro Leu Xaa Xaa Met Met Asp Asn Ile Arg Lys Arg			
30	35	40	
gaa act gaa gtg gtc taacactcta taraaaaatga acaaaaatctc tgaaaagcagc			467
Glu Thr Glu Val Val			
45			
tcaaacctctt ctgaraaaaa aaatatattc tgaggccaac tgttgctaca aaacaaattc			527
tgactgaatg gttaaaaacat ttctagtara aggggaaaaaa aaakttaaac atgcactgtt			587
tgtgtgtata sccatttcat taaatataca gtaaaactyc aaaaaaaaaaa aa			639
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score 3.79999995231628			
seq TFINITLWLGSCL/QR			
<221> polyA_site			
<222> 762..772			
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acagctgggg ctttgtcttc tttattgcta ggagaatgta gcaatagaag ttctcatcg			60
cctgtattgc acctttgggt ttaaggactg gacccagagt tcctgaaagc caaactccat			120
aagctgctca gtaagttcca agcacatagc cggctkhggg atgcgattcg gtcgaggtct			180
gttgaatgaa ggttagacgca gcaggcagtt tgccttacc agtgcacctgg aagacgttgg			240
cacttcctga gtgagctcac ttacccccc tgaatggta ggc atg gat gaa tat			295
Met Asp Glu Tyr			
-30			
tcc tgg tgg tgc cac gtc tta gag gtc gta aag ggt caa atg ttt act			343
Ser Trp Trp Cys His Val Leu Glu Val Val Lys Gly Gln Met Phe Thr			
-25	-20	-15	
ttt att aat att aca tta tgg ctt ggt tct ctg tgt cag cga ttt ttc			391
Phe Ile Asn Ile Thr Leu Trp Leu Gly Ser Leu Cys Gln Arg Phe Phe			
-10	-5	1	
tat gcc tcg ggt act tat ttc cta ata tat atc agc aca gta acg cct			439
Tyr Ala Ser Gly Thr Tyr Phe Leu Ile Tyr Ile Ser Thr Val Thr Pro			
5	10	15	20
agc tgg agg ctt tgt ctt gtt agt tgataaatta gtggtaacag gtagatttgg			493
Ser Trp Arg Leu Cys Leu Val Ser			
25			
ttaccccca aagtgctggg attrcagacg tgagccaccg cgccctggccg aaacaattct			553
tttggaaagag agaagtctcc ctgtgttgcg caggctggtc tcagactcct ggggtcaagt			613
gagccctctg ctttcgcctc ctaaagtgtc gggattacag gcgtgagccca ccgcacccgg			673
acagatgtgt tgatTTaaa gtggtatga ggcctgagcc ctggagttt agaccagcct			733
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<212> DNA			

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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 162..671

&lt;221&gt; sig\_peptide

&lt;222&gt; 162..398

&lt;223&gt; Von Heijne matrix

score 4.09999990463257

seq QGVLFICFTCARs/FP

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&lt;222&gt; 805..810

&lt;221&gt; polyA\_site

&lt;222&gt; 830..840

&lt;400&gt; 278

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ctgcaacgcg cgtgggagc gggggctctg ggcggaaaca aaatcacagg atgtcagagg	120
atgtttcccg ggaagaactg ggataaagggt gtcccagcac c atg gag gac ccg aac	176
Met Glu Asp Pro Asn	
-75	
cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt ccc	224
Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser Pro	
-70            -65            -60	
cag agc cca gga ggc aac atc tgc cac ctg ggg gcc ccg aag tgc acc	272
Gln Ser Pro Gly Asn Ile Cys His Leu Gly Ala Pro Lys Cys Thr	
-55            -50            -45	
cgc tgc ctc atc acc ttc gca gat tcc aag ttc cag gag cgt cac atg	320
Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe Gln Glu Arg His Met	
-40            -35            -30	
aag cgg gag cac cca gcg gac ttc gtg gcc cag aag ctg cag ggg gtc	368
Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln Lys Leu Gln Gly Val	
-25            -20            -15	
ctc ttc atc tgc ttc acc tgc gcc tcc ttc ccc tcc tcc aaa gcc	416
Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe Pro Ser Ser Lys Ala	
-10            -5            1            5	
ckr rkc acc cac car cgc agc cac ggt cca rcc gcc aag ccc acc ctg	464
Xaa Xaa Thr His Gln Arg Ser His Gly Pro Xaa Ala Lys Pro Thr Leu	
10            15            20	
ccg gtt gca acc act act gcc car ccc acc ttc cct tgt cct gac tgt	512
Pro Val Ala Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp Cys	
25            30            35	
ggc aaa acc ttt ggg cag gct gtt tct ctg arg cgg cac csc caa atr	560
Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Xaa Arg His Xaa Gln Xaa	
40            45            50	
cat gar gtc cgt gcc cct cct ggc acc ttc gcc tgc aca rad tgc ggt	608
His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Xaa Cys Gly	
55            60            65            70	
cag gac ttt gct car gaa rca ggg ctg cat caa cac tac att cgg cat	656
Gln Asp Phe Ala Gln Glu Xaa Gly Leu His Gln His Tyr Ile Arg His	
75            80            85	
gcc cgg ggg gga ctc tgagttcagc ttaaggctct ccacggtgac gggtggtct	711
Ala Arg Gly Gly Leu	
90	
gtggctggta ggactcaccc atgatatggg gtgcaggaac tctggggcc ctgaaggatt	771
tgcttccttc ccctggaaag gcagagggt ctaataaaag aggaccaka agattctaa	831
aaaaaaaaaa	840

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<221> sig\_peptide  
<222> 63..308  
<223> Von Heijne matrix  
score 4.4000009536743  
seq NLPHLQVVGLTWG/HI

<221> polyA\_signal  
<222> 808..813

<221> polyA\_site  
<222> 829..840

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ga atg tat gtd tgg ccc tgt gct gtg gtc ctg gcc cag tac ctt tgg 107  
Met Tyr Val Trp Pro Cys Ala Val Val Leu Ala Gln Tyr Leu Trp  
-80 -75 -70  
ttt cac aga aga tct ctg cca ggc aag gcc atc tta gag att gga gct 155  
Phe His Arg Arg Ser Leu Pro Gly Lys Ala Ile Leu Glu Ile Gly Ala  
-65 -60 -55  
gga gtg agc ctt cca gga att ttg gct gcc aaa tgt ggt gca gaa gta 203  
Gly Val Ser Leu Pro Gly Ile Leu Ala Ala Lys Cys Gly Ala Glu Val  
-50 -45 -40  
ata ctg tca gac agc tca gaa ctg cct cac tgt ctg gaa gtc tgt cgg 251  
Ile Leu Ser Asp Ser Ser Glu Leu Pro His Cys Leu Glu Val Cys Arg  
-35 -30 -25 -20  
caa agc tgc caa atg aat aac ctg cca cat ctg cag gtg gta gga cta 299  
Gln Ser Cys Gln Met Asn Asn Leu Pro His Leu Gln Val Val Gly Leu  
-15 -10 -5  
aca tgg ggt cat ata tct tgg gat ctt ctg gct cta cca cca caa gat 347  
Thr Trp Gly His Ile Ser Trp Asp Leu Leu Ala Leu Pro Pro Gln Asp  
1 5 10  
att atc ctt gca tct gat gtg ttc ttt gaa cca gaa rat ttt gaa gac 395  
Ile Ile Leu Ala Ser Asp Val Phe Phe Glu Pro Glu Xaa Phe Glu Asp  
15 20 25  
att ttg gct aca ata tat ttt ttg atg cac aar aat ccc aag gtc caa 443  
Ile Leu Ala Thr Ile Tyr Phe Leu Met His Lys Asn Pro Lys Val Gln  
30 35 40 45  
ttg tgg tct act tat caa gtt agg art gct gac tgg tca ctt gaa gct 491  
Leu Trp Ser Thr Tyr Gln Val Arg Xaa Ala Asp Trp Ser Leu Glu Ala  
50 55 60  
tta ctc tac aaa tgg gat atg aaa tgt gtc cac att cct ctt gag tct 539  
Leu Leu Tyr Lys Trp Asp Met Lys Cys Val His Ile Pro Leu Glu Ser  
65 70 75  
ttt gat gca gac aaa gaa rat ata gca gaa tct acc ctt cca gga aga 587  
Phe Asp Ala Asp Lys Glu Xaa Ile Ala Glu Ser Thr Leu Pro Gly Arg  
80 85 90  
cat aca gtt gaa atg ctg gtc att tcc ttt gca aag gac agt ctc 632  
His Thr Val Glu Met Leu Val Ile Ser Phe Ala Lys Asp Ser Leu  
95 100 105  
tgaattatac ctacaacctg ttctggaca gtatcaatac tgatgagcaa cctggcacac 692  
aaactatgag cagaccacctt cagcttgaga atgcagtggg tctgaagatg gtcaagtctg 752

tttgccttar attttgatgt cacctagaca acacttaaac tcatatgaaa caaaaattaa 812  
 aatacgtatt acaagcaaaa aaaaaaaaa 840

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 seq LVILSLKSQTLDA/ET

<221> polyA\_signal  
 <222> 821..826

<221> polyA\_site  
 <222> 838..849

<400> 280

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Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro		
-60	-55	-50

tgg aac cgt gtg aga atc cct aag gcg ggg aac cgc agc gca gtg aca	101	
Trp Asn Arg Val Arg Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr		
-45	-40	-35

gtg cag aac ccc ggc gcg gcc ctt gac ctt tgc att gca gct gta att	149	
Val Gln Asn Pro Gly Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile		
-30	-25	-20

aaa gaa tgc cat ctc gtc ata ctg tcg ctg aag agc caa acc tta gat	197	
Lys Glu Cys His Leu Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp		
-15	-10	-5

gca gaa aca gat gtg tta tgt gca gtc ctt tac agc aat cac aac aga	245		
Ala Glu Thr Asp Val Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg			
1	5	10	15

atg ggc cgc cac aaa ccc cat ttg gcc ctc aaa cag gtt gag caa tgt	293	
Met Gly Arg His Lys Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys		
20	25	30

tta aag cgt ttg aaa aac atg aat ttg gag ggc tca att caa gac ctg	341	
Leu Lys Arg Leu Lys Asn Met Asn Leu Glu Gly Ser Ile Gln Asp Leu		
35	40	45

ttt gag ttg ttt tct tcc aag taagtaagt gtccarttgc ttttgtatgt	392
Phe Glu Leu Phe Ser Ser Lys	
50	

ggtgggctgg gaactcaatg tcttgtgatc kcccttwgga ttktctakg ctygckgttg	452
aatataacc aattataaccw cagctgtaka aatwttgtt taatgtgggg taccygggt	512
ktgtggtaat cttctgacat tgatctatgg gartgactgg tgtgacattg aaatctgggt	572
catggtagat tatattaaaa catcagtggg ctgttattgt gcttaactac ctcaagttga	632
gcttaaagca agtcttcaact tgaaaactgc tatagaaatg ctttatattt aaaaatgaaa	692
gtaatgggar mttgcacata gctgaaaatg tgaagggtcg cccagggagg amatggaagc	752
tctgtgcttc ttctgccata cttgccata tgcattcttt tgtttcaatc ctttgtcata	812
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<212> DNA  
<213> Homo sapiens

<220>  
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<222> 21..503

<221> sig\_peptide  
<222> 21..344  
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score 5.30000019073486  
seq ACMTLTASPGVFP/SL

<221> polyA\_signal  
<222> 1305..1310

<221> polyA\_site  
<222> 1330..1341

<400> 281
aaacaactcc gaaaagtaca atg acc agc ggg cag gcc cga gct tcc wyc cag 53
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-105 -100
tcc ccc cag gcc ctg gag gac tcg ggc ccg gtg aat atc tca gtc tca 101
Ser Pro Gln Ala Leu Glu Asp Ser Gly Pro Val Asn Ile Ser Val Ser
-95 -90 -85
atc acc cta acc ctg gac cca ctg aaa ccc ttc gga ggg tat tcc cgc 149
Ile Thr Leu Thr Leu Asp Pro Leu Lys Pro Phe Gly Gly Tyr Ser Arg
-80 -75 -70
aac gtc acc cat ctg tac tca acc atc tta ggg cat cag att gga ctt 197
Asn Val Thr His Leu Tyr Ser Thr Ile Leu Gly His Gln Ile Gly Leu
-65 -60 -55 -50
tca ggc agg gaa gcc cac gag gag ata aac atc acc ttc acc ctg cct 245
Ser Gly Arg Glu Ala His Glu Glu Ile Asn Ile Thr Phe Thr Leu Pro
-45 -40 -35
aca gcg tgg agc tca gat gac tgc gcc ctc cac ggt cac tgt gag cag 293
Thr Ala Trp Ser Ser Asp Asp Cys Ala Leu His Gly His Cys Glu Gln
-30 -25 -20
gtg gta ttc aca gcc tgc atg acc ctc acg gcc agc cct ggg gtg ttc 341
Val Val Phe Thr Ala Cys Met Thr Leu Thr Ala Ser Pro Gly Val Phe
-15 -10 -5
ccg tca ctg tac agc cac cgc act gtg ttc ctg aca cgt aca gca acg 389
Pro Ser Leu Tyr Ser His Arg Thr Val Phe Leu Thr Arg Thr Ala Thr
1 5 10 15
cca cgc tct ggt aca aga tct tca caa ctg cca gag atg cca aca caa 437
Pro Arg Ser Gly Thr Arg Ser Ser Gln Leu Pro Glu Met Pro Thr Gln
20 25 30
aat acg ccc aaa att aca atc ctt tct ggt gtt ata agg ggg cca ttg 485
Asn Thr Pro Lys Ile Thr Ile Leu Ser Gly Val Ile Arg Gly Pro Leu
35 40 45
gaa aag tct atc atg ctt taaatcccaa gcttacagtg attgttccag 533
Glu Lys Ser Ile Met Leu
50
atgatgaccg ttcatataata aatttgcata tcatacgacac cagttacttc ctctttgtga 593
tgggtataac aatgtttgc tatgtgtta tcaaggccag accttagcaaa ttgcgtcaga 653
gcaatcctga attttgtccc gagaagggtgg ctttggctga agcctaattc cacagctcct 713
tggttttgc gagagactga gagaaccata atccttgccct gctgaacccca gcctggccct 773
ggatgtctg tgaatacatt atcttgcgtat gttgggttat tccagccaaa gacattcaa 833
gtgcctgtaa ctgatttgcata tataattata aaaatctatt cagaaattgg tccaaataatg 893
cacgtgtttt gcccctgggtt cagccagagc ccttcaaccc caccttggac ttgaggacct 953

acctgatggg acgtttccac gtgtctctag agaaggatcc tggatcttagc tggtcacgac	1013
gatgtttca ccaaggtcac aggagcattg cgtcgctgat ggggttgaag tttgggttgg	1073
ttcttgtttc agcccaatat gtagagaaca ttgaaacag tctgcaccc ttgatacgta	1133
ttgcatttcc aaagccacca atccatttt tggattttat gtgtctgtgg cttaataatc	1193
atagtaacaa caataatacc ttttctcca ttgtgttc aggaaacata ccttaaggaaa	1253
ttttgtttt gttttgttt ttgtttctt tatgaagaaaa aaataaaaata	1313
gtcacatTTT aatacyaaaa aaaaaaaaaamc h	1344

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<212> DNA  
<213> Homo sapiens

<220>  
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<222> 1..201

<221> sig\_peptide  
<222> 1..63  
<223> Von Heijne matrix  
score 5.09999990463257  
seq LLLKIWLLQRPES/QE

<221> polyA\_signal  
<222> 637..642

<221> polyA\_site  
<222> 660..671

<400> 282  
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Met Leu Gly Gly Asp His Arg Ala Leu Leu Leu Lys Ile Trp Leu Leu  
-20                -15                -10  
caa agg cca gag tca cag gaa gga ctt ctt cca ggg aga tta gtg gtg      96  
Gln Arg Pro Glu Ser Gln Glu Gly Leu Leu Pro Gly Arg Leu Val Val  
-5                1                5                10  
atg gag agg aga gtt aaa aat gac ctc atg tcc ttc ttg tcc acg gtt      144  
Met Glu Arg Arg Val Lys Asn Asp Leu Met Ser Phe Leu Ser Thr Val  
15                20                25  
ttg ttg agt ttt cac tct tct aat gca agg gtc tca cac tgt gaa cca      192  
Leu Leu Ser Phe His Ser Ser Asn Ala Arg Val Ser His Cys Glu Pro  
30                35                40  
ctt agg atg tgatcacttt caggtggcca ggaatgttga atgtctttgg      241  
Leu Arg Met  
45  
ctcagttcat ttaaaaaaga tatctattt aagttctca rarttgatcata tatgtttcac      301  
agtacaggat ctgtacataa aagtttctt cctaaaccat tcaccaagag ccaatatcta      361  
ggcattttct tggtagcaca aattttctta ttgcttaraa aattgtcctc cttgttattt      421  
ctgtttgtaa racttaagtg agttaggtct ttaaggaaa caacgctccct ctgaaatgct      481  
tgtctttttt ctgttgccga aatarctgtt ccttttcgg gagttaratg tatarartgt      541  
ttgtatgtaa acatttctt taggcacac catgaacaaa gatatatttt ctatattttt      601  
attatatgtg cacttcaaga agtcaactgtc agagaaataa agaattgtct taaatgtcaa      661  
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<212> DNA  
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<221> sig_peptide
<222> 39..134
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score 6.0999990463257
seq LPLLTSALHGLQQ/QH

<221> polyA_signal
<222> 1566..1571

<221> polyA_site
<222> 1587..1597

<400> 283
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Met Ile Xaa Leu Arg Asp
-30
aca gct gcc tcc ctc cgc ctt gag aga gac aca agg cag ttg cca ctg      104
Thr Ala Ala Ser Leu Arg Leu Glu Arg Asp Thr Arg Gln Leu Pro Leu
-25          -20          -15
ctc acc agt gcc ctg cac gga ctg cag cag cac cca gcc ttc tct      152
Leu Thr Ser Ala Leu His Gly Leu Gln Gln His Pro Ala Phe Ser
-10          -5           1           5
ggt gtg gca cgg ctg gcc aag cgg tgg gtg cgt gcc cag ctt ctt ggt      200
Gly Val Ala Arg Leu Ala Lys Arg Trp Val Arg Ala Gln Leu Leu Gly
-10          10          15          20
gag ggt ttc gct gat gag agc ctg gat ctg gtg gcc gct gcc ctt ttc      248
Glu Gly Phe Ala Asp Glu Ser Leu Asp Leu Val Ala Ala Leu Phe
-25          30          35
ctg cac cct gag ccc ttc acc cct ccg agt tcc ccc cag gtt ggc ttc      296
Leu His Pro Glu Pro Phe Thr Pro Pro Ser Ser Pro Gln Val Gly Phe
-40          45          50
ctt cga ttc ctt ttc ttg gta tca acg ttt gat tgg aag aac aac ccc      344
Leu Arg Phe Leu Phe Leu Val Ser Thr Phe Asp Trp Lys Asn Asn Pro
-55          60          65          70
ctc ttt gtc aac ctc aat aat gag ctc act gtg gag gag cag gtg gar      392
Leu Phe Val Asn Leu Asn Asn Glu Leu Thr Val Glu Glu Gln Val Glu
-75          80          85
atc cgc agt ggc ttc ctg gca gct cgg gca cag ctc ccc gtc atg gtc      440
Ile Arg Ser Gly Phe Leu Ala Ala Arg Ala Gln Leu Pro Val Met Val
-90          95          100
att gtt acc ccc caa rac cgc aaa aac tct gtg tgg aca cag gat gga      488
Ile Val Thr Pro Gln Xaa Arg Lys Asn Ser Val Trp Thr Gln Asp Gly
-105         110         115
ccc tca gcc car atc ctg cag cag ctt gtg gtc ctg gca gct gaa scc      536
Pro Ser Ala Gln Ile Leu Gln Gln Leu Val Val Leu Ala Ala Glu Xaa
-120         125         130
ctg ccc atg tta rar aas cag ctc atg gat ccc cgg gga cct ggg gac      584
Leu Pro Met Leu Xaa Xaa Gln Leu Met Asp Pro Arg Gly Pro Gly Asp
-135         140         145         150
atc agg aca gkg ttc cgg ccc ttg gac att tac gac gtg ctg att      632
Ile Arg Thr Xaa Phe Arg Pro Pro Leu Asp Ile Tyr Asp Val Leu Ile
-155         160         165
cgc ctg tct cct cgc cat atc ccg cgg cac cgc cag gct gtg gac tcr      680
Arg Leu Ser Pro Arg His Ile Pro Arg His Arg Gln Ala Val Asp Ser
-170         175         180
cca gct gcc tcc ttc tgc cgg ggc ctg ctc agc cag ccg ggg ccc tca      728
Pro Ala Ala Ser Phe Cys Arg Gly Leu Leu Ser Gln Pro Gly Pro Ser

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185	190	195	
tcc ctg atg ccc gtg ctg ggc tak gat cct cct cag ctc tat ctg acg			776
Ser Leu Met Pro Val Leu Gly Xaa Asp Pro Pro Gln Leu Tyr Leu Thr			
200	205	210	
cag ctc arg gag gcc ttt ggg gat ctg gcc ctt ttc tat gac cag			824
Gln Leu Xaa Glu Ala Phe Gly Asp Leu Ala Leu Phe Phe Tyr Asp Gln			
215	220	225	230
cat ggt gga gag gtg att ggt gtc ctc tgg aag ccc acc agc ttc cag			872
His Gly Gly Glu Val Ile Gly Val Leu Trp Lys Pro Thr Ser Phe Gln			
235	240	245	
ccg cag ccc ttc aag gcc tcc agc aca aag ggg cgc atg gtg atg tct			920
Pro Gln Pro Phe Lys Ala Ser Ser Thr Lys Gly Arg Met Val Met Ser			
250	255	260	
cga ggt ggg gag cta gta atg gtg ccc aat gtt gaa gca atc ctg gag			968
Arg Gly Gly Glu Leu Val Met Val Pro Asn Val Glu Ala Ile Leu Glu			
265	270	275	
gac ttt gct gtg ctg ggt gaa ggc ctg gtg cag act gtg gag gcc cga			1016
Asp Phe Ala Val Leu Gly Glu Leu Val Gln Thr Val Glu Ala Arg			
280	285	290	
agt gag agg tgg act gtg tgatcccagc tctggagcaa gctgttagacg			1064
Ser Glu Arg Trp Thr Val			
295	300		
gacagcagga cattggacct ctagagaag atgtcagtag gatgacaccttcc acccttccttg			1124
gacatgaatc ctccatggag ggcctgtgg ctgaacatgc tgaatcatct ccaacaaaac			1184
ccagccccaa ctttctctct gatgctccag cattggggca ggggcatggt ggccccatgta			1244
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cccaggagat ccatccaccc attagccctg ggcctggacc tccctgcgtat ttcccactcc			1364
tttcttagtc ttcttccaga aacagagaag gggatgtgtg octggagag gctctgtctc			1424
cttcctgctg ccaggacctg tgccttagact tagcatgcc ttcactgcag tgcaggcct			1484
ttagatggga cccagcgaaa atgtggccct tctgagtcac atcaccgaca ctgagcgtg			1544
gaaaggggct atatgtgtat gaatagacca cattgaagga gaaaaaaaaaa aaamcch			1601

<210> 284  
<211> 1206  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 69..263

<221> sig\_peptide  
<222> 69..125  
<223> Von Heijne matrix  
score 3.90000009536743  
seq ALSMSSFSFHSSS/CS

<221> polyA\_signal  
<222> 1173..1178

<221> polyA\_site  
<222> 1196..1205

<400> 284  
acatttgtga ctttaccaat accctccag ttcttgatag acagctgttag gttgctgggt 60  
tcaagaat atg ggt ggg ata tgg aat gct ctt tca atg tct agc ttc agt 110  
Met Gly Gly Ile Trp Asn Ala Leu Ser Met Ser Ser Phe Ser  
-15 -10  
ttt cat tca tcc tcc tgc tca gca ctg tca gcc aag agc tta ctc agc 158  
Phe His Ser Ser Ser Cys Ser Ala Leu Ser Ala Lys Ser Leu Leu Ser

-5	1	5	10	
aga cac cac ata ctg cag cag ttc cta gtg aga aaa tct gtg cca cta				206
Arg His His Ile Leu Gln Gln Phe Leu Val Arg Lys Ser Val Pro Leu				
15	20	25		
gaa aat gct tca ctt cca ttt cct cac ctg ggc agt tct ctg ttt aaa				254
Glu Asn Ala Ser Leu Pro Phe Pro His Leu Gly Ser Ser Leu Phe Lys				
30	35	40		
att gtg ggc tgatttggtc ttccctctcct cctcccactg ttactgccct				303
Ile Val Gly				
45				
gcagcccttg ttccagggtgtta cagaccctta ttctggcctc tagtgtcctt gtctgtcatg				363
acacaccctt ccggccaaat acctctgacc ccaaggctgg aatggggctg gtaggarata				423
agtttgccta ctcataartca tgcctttctt cttggcacct gcttccctgc ggtgtccctca				483
aatggatttc tgggtggcag tggartgatt gcatgaattt ttctgtaaaca cattaacttt				543
gtattattat taaggartt tgaraaagct ttgcttataa tgtcaaggca aggaggtaaa				603
aactggagcc caaakaaatt cccttagggc aagattatgt tataataraa aattgaattt				663
cctgaggcag tggctgccac ccctttcar atgttttagtc ctgcaaatacg catctttctt-				723
gtagtctgtg acatggatgg ggatgttagg gccccttaggg gcaaggggac taaaactaaat				783
caakttgagt tttttccag caggggttar gggaggtact csctgttgc atttgacact				843
araaaagtaat ctttttaca aaactgttt tctaggtggg tggaaagtga aactgccaca				903
tccttgcgg ttttagtccaa raracattt gcaacaacag taratgtccg ggaaaaat				963
ctgtctttt attatgaaaa actatgttaa gggggaaaaat gtggattatg gtaaccarag				1023
gaatccctas cctgttttc cttaraarac ttgttttagtg ttttatcara cgtctgtgt				1083
agttgtarac aggaaagctt gtgaraaaaa caccacatgg ascctgtaaa tgaaaaat				1143
caacctgtaa agcattctt gaaatggcca gtaaaaagggttttaccat ttaaaaaaaaaa				1203
aat				1206

<210> 285	
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<212> DNA	
<213> Homo sapiens	
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<222> 115..285	
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<222> 115..204	
<223> Von Heijne matrix	
score 3.70000004768372	
seq SMMLLTVYGGYLC/SV	
<221> polyA_signal	
<222> 505..510	
<221> polyA_site	
<222> 525..536	
<400> 285	
acgagtgcgt cggtcggtctg tgctggaaag ttgcgttagac agtggcctcg agaccctgcc	60
tgcctgagga ggccctcggtt ggatgcgaag gagctgcagc atccaggaa caag atg	117
Met	
-30	
cca act ggc aag cag cta gct gac att ggc tat aag acc ttc tct acc	165
Pro Thr Gly Lys Gln Leu Ala Asp Ile Gly Tyr Lys Thr Phe Ser Thr	
-25 -20 -15	
tcc atg atg ctt ctc act gtg tat ggg ggg tac ctc tgc agt gtc cga	213
Ser Met Met Leu Leu Thr Val Tyr Gly Tyr Leu Cys Ser Val Arg	
-10 -5 1	
gtc tac cac tat ttc cag tgg cgc agg gcc cag cgc cag gcc gca gaa	261

Val Tyr His Tyr Phe Gln Trp Arg Arg Ala Gln Arg Gln Ala Ala Glu			
5	10	15	
gaa cag aag dac tca gga atc atg tagaactggg gggcttttc tcctgagcar			315
Glu Gln Lys Xaa Ser Gly Ile Met			
20	25		
asakgcccaa ggcatgctgt ggagagactt cacctgccac cattccagg tcaacaggac			375
tagagcggtt taggtttca aaccctgttg gaagaaaagtg cccatggttt ctctggttct			435
gccarttga cagtttatgg argctttga atcgttaatar caatgtgagg gtgargtaca			495
cctacagaca ttaataatt tgctgtgtca aaaaaaaaaa a			536

&lt;210&gt; 286

&lt;211&gt; 529

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; 90..344

&lt;221&gt; sig\_peptide

&lt;222&gt; 90..140

&lt;223&gt; Von Heijne matrix

score 8.19999980926514

seq LLLITAILAVAVG/FP

&lt;221&gt; polyA\_signal

&lt;222&gt; 500..505

&lt;221&gt; polyA\_site

&lt;222&gt; 515..527

&lt;400&gt; 286

aatatrarac agctacaata ttccagggcc artcaattgc catttctcat aacagcgta	60
gagagaaaga actgactgar acgttttag atg aag aaa gtt ctc ctc ctg atc	113
Met Lys Lys Val Leu Leu Leu Ile	
-15	-10

aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag	161	
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln		
-5	1	5

gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr	209	
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly		
10	15	20

wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att	257	
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile		
25	30	35

cca ttt cca aga ttt cca tgg ttt aga cgt aat ttt cct att cca ata	305		
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Asn Phe Pro Ile Pro Ile			
40	45	50	55

cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaaacaaraa	354	
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys		
60	65	

ggaaaaagtca crataaacct ggtcacctga aattgaaatt gagccacttc cttgaaraat	414
caaaattcct gtaataaaaa raaaaacaaa tggtaattgaa atagcacaca gcattctcta	474
gtcaatatct ttatgtatct tcttaataaa acatgaaagc aaaaaaaaaa aaacc	529

&lt;210&gt; 287

&lt;211&gt; 493

&lt;212&gt; DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 57..311

<221> sig\_peptide

<222> 57..107

<223> Von Heijne matrix

score 8.19999980926514

seq LLLITAILAVAVG/FP

<221> polyA\_signal

<222> 467..472

<221> polyA\_site

<222> 462..493

<400> 287

aacttgc	cat ttctcataac	agcg	tca	gag agaaagaact	gactgaaacg	tttgag	atg	59
Met								
aag	aaa gtt ctc ctc ctg atc aca gcc atc ttg gca gtg gct gtt ggt							107
Lys	Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val Gly							
-15	-10	-5						
ttc	cca gtc tct caa gac cak gaa cga gaa aaa aga agt atc agt gac							155
Phe	Pro Val Ser Gln Asp Xaa Glu Arg Glu Lys Arg Ser Ile Ser Asp							
1	5	10	15					
agc	gat gaa tta gct tca ggg ttt ttt gtg ttc cct tac cca tat cca							203
Ser	Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr Pro							
20	25	30						
ttt	cgc cca ctt cca cca att cca ttt cca aga ttt cca tgg ttt aga							251
Phe	Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe Arg							
35	40	45						
cgt	aat ttt cct att cca ata cct gaa tct gcc cct aca act ccc ctt							299
Arg	Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro Leu							
50	55	60						
ccg	agc gaa aag taaacaagaa ggaaaagtca cgataaacct ggtcacctga							351
Pro	Ser Glu Lys							
65								
aattgaaatt	gagccacttc cttgargaat caaaattcct gttataaaaa gaaaaacaaa							411
tgtaattgaa	atagcacaca gcattctcta gtcaatatct ttagtgatct tctttaataa							471
acatgaaagc	aaaaaaaaaa aa							493

<210> 288

<211> 521

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 96..302

<221> sig\_peptide

<222> 96..182

<223> Von Heijne matrix

score 5

seq ELSLLPSSLWVLA/TS

<221> polyA\_site

<222> 501..514

<400> 288  
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 tctcatccag cggctgcgga actgggcgtc cgggc atg acc tgc agg gga agc 113  
 Met Thr Cys Arg Gly Ser  
 -25  
 tgc agc tac gct acc agg aga tct cca agc gaa ctc agc ctc ctc cca 161  
 Cys Ser Tyr Ala Thr Arg Arg Ser Pro Ser Glu Leu Ser Leu Leu Pro  
 -20 -15 -10  
 agc tcc ctg tgg gtc cta gcc aca agc tct cca aca att act att gca 209  
 Ser Ser Leu Trp Val Leu Ala Thr Ser Ser Pro Thr Ile Thr Ile Ala  
 -5 1 5  
 ctc gcg atg gcc gcc ggg aat ctg tgc ccc ctt cca tca tca tkt cgt 257  
 Leu Ala Met Ala Ala Gly Asn Leu Cys Pro Leu Pro Ser Ser Xaa Arg  
 10 15 20 25  
 crc aaa agg cgc tgg tgt cag gca asc car caa ara gct ctg ctg 302  
 Xaa Lys Arg Arg Trp Cys Gln Ala Xaa Gln Gln Xaa Ala Leu Leu  
 30 35 40  
 tagctgccac tgaaaaraag gcgggtactc cagctcctcc cataaaagagg tggagctgt 362  
 cctcggacca gccttacctg tgacactgca ccctcacggc caccggacta cttgcctcc 422  
 ttggatttcc tccagggaga atgtgaccta atttatgaca aatacgtara gtcaggtat 482  
 cacttctagt ttactttaa aaaataaaaa aatagagac 521

<210> 289  
<211> 811  
<212> DNA  
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<220>  
<221> CDS  
<222> 161..526  
<221> sig\_peptide  
<222> 161..328  
<223> Von Heijne matrix  
score 4.1999980926514  
seq XSPLLTALLGQC/SL  
<221> polyA\_site  
<222> 799..811  
<400> 289  
aaaaaaaaattgc agtgctgaag acactggacc cgcaaaaggc tgcctccc aaacctggga 60  
ttctgggctc actgagttca cctgcgagtc agccctacct gcactgctct ggtctagttac 120  
aaacaggctg ctggcattga ggtctgctac aaaaanarta atg gtc cca tgg ccc 175  
Met Val Pro Trp Pro  
-55  
agg ggc aag gtg aaa act gct cct att ccc atc tct agg ttt cct ttc 223  
Arg Gly Lys Val Lys Thr Ala Pro Ile Pro Ile Ser Arg Phe Pro Phe  
-50 -45 -40  
ctc cct acc cac gac cca ccc acc cca gca cat tgg tct cca gca tct 271  
Leu Pro Thr His Asp Pro Pro Thr Pro Ala His Trp Ser Pro Ala Ser  
-35 -30 -25 -20  
cat cag cag ttt aaa cat kkg tca ccc ctc ctc act ttg gcc ctg ctg 319  
His Gln Gln Phe Lys His Xaa Ser Pro Leu Leu Thr Leu Ala Leu Leu  
-15 -10 -5  
ggt cag tgc tct ctg ttc arc aat ttg agg aaa aaa ctt gca ggg caa 367  
Gly Gln Cys Ser Leu Phe Xaa Asn Leu Arg Lys Lys Leu Ala Gly Gln  
1 5 10  
aaa gca aaa aaa tta cct tcc ttc tcc agc ctg ccc ctg aca ctc tgg 415

Lys Ala Lys Lys Leu Pro Ser Phe Ser Ser Leu Pro Leu Thr Leu Trp			
15	20	25	
cca tta act cct caa ttt gct gag ctc act aca gtg gca caa aaa aaaa			463
Pro Leu Thr Pro Gln Phe Ala Glu Leu Thr Thr Val Ala Gln Lys Lys			
30	35	40	45
ttg agg tgg tcc ggg acc cta ggt tgg ggt cca gtt ccc agc tgg gtt			
Leu Arg Trp Ser Gly Thr Leu Gly Trp Gly Pro Val Pro Ser Trp Val			
50	55	60	
caa ttt ttt tta ggg tgaatggagg garagttggg gactgaaaaas ccttcaaara			566
Gln Phe Phe Leu Gly			
65			
caatgttatt acagcaktct ccccttatcc aaaktttcctt ttcccttgadt tttagttgc			626
tatggtaaac cgcttgaaaa atakttgaac acagtacaat aaratatttt gaggctggga			686
ktgggtggctc atgcctgtaa taatcccagg actttgtgar accaaktttg aaggatcact			746
tgaacccagg aktttgarac cascctgggc aacatrgtra gacctcatct ctacaaaaaa			806
aaaaaa			811

<210> 290			
<211> 625			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> 210..332			
<221> sig_peptide			
<222> 210..299			
<223> Von Heijne matrix			
score 8.10000038146973			
seq ITCLLAFWVPASC/IQ			
<221> polyA_signal			
<222> 594..599			
<221> polyA_site			
<222> 613..625			
<400> 290			
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attatcgta cagccctcta ctgccttctc atcatgtggc cagagctatc ttccctaaaa		120	
atgcattgca tagttatca agtcaactctc tggctaaaaa cttcccttgg ctccctgtg		180	
ccctcaggat aaagtcttggc cccctcage atg gct tgt gag act cat ggt gtc		233	
Met Ala Cys Glu Thr His Gly Val			
-30	-25		
ctt gtc cct gct cac ctc tct ggt ctc atc act tgc ctt ctt gca ttc		281	
Leu Val Pro Ala His Leu Ser Gly Leu Ile Thr Cys Leu Leu Ala Phe			
-20	-15	-10	
tgg gtc cca gcc tcc tgt atc cag aga tgc agt ggc tct cca ttg cca		329	
Trp Val Pro Ala Ser Cys Ile Gln Arg Cys Ser Gly Ser Pro Leu Pro			
-5	1	5	10
ctc tgattcctcc ttcttttgg tcacagagaa agggtacttt ctctgtcaaa		382	
Leu			
tctcaactta gacttgactt cctccaagga gctttggcta tactctctcc cwcgacccccc		442	
accctggcat actacacara tcactctggg ctcacttgcc tgcctaatgg tcatctcccc		502	
agtaaactgt aagctccttg agggcaagga ttgtgttgaa attttgtat taacagtgcc		562	
tggcttggtg cctggcacct aaaaagcact caataaatgt ttgtttaatg aaaaaaaaaaa		622	
aaa		625	

<210> 291  
<211> 684  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 212..361

<221> sig\_peptide  
<222> 212..319  
<223> Von Heijne matrix  
score 4.0999990463257  
seq HWLFLASLSGIKT/YQ

<221> polyA\_signal  
<222> 650..655

<221> polyA\_site  
<222> 673..684

<400> 291

atccccawns cactctctca cagagactgt tcttttcctt ctgagaccct actccagctt	60	
gttagttctaa atctgtgatt atgcactgtc tgtcttcctc ttgaggtag gggccatssc	120	
ttttgttctc tgctatgctc aggaccaga tcaaaggagc tcagtaacta tttacaggcg	180	
tacatcatat gtggaggaca cttatgctgt g atg gcc cca cac aca gct tcc	232	
Met Ala Pro His Thr Ala Ser		
-35	-30	
ttt ggg gtc tgt ccc ctg ctc tcc gtt acc cgc gtg gta gcc act gag	280	
Phe Gly Val Cys Pro Leu Leu Ser Val Thr Arg Val Val Ala Thr Glu		
-25	-20	-15
cac tgg ctc ttc ctg gct tca ctc tct ggc atc aaa act tat cag tcc	328	
His Trp Leu Phe Leu Ala Ser Leu Ser Gly Ile Lys Thr Tyr Gln Ser		
-10	-5	1
tac atc tca gtc ttt tgc aag gtg aca ctt atc tgattaccta attcacacra	381	
Tyr Ile Ser Val Phe Cys Lys Val Thr Leu Ile		
5	10	
aggtgttaat ggtggtaatg gcataktatt tattacccca ggggacccak aacggtgta	441	
tcaaaaacata tcattcccca gtggttaaa actctggtag ctttccargg aatccaaagt	501	
ggaatccagt ctcccttagct gawttcacag gggcccgtct gcacaacttg gcttctgtcg	561	
gcttccctan ccctgacttc ccaaggctta gtcatcaccc tctctccac ccagggctca	621	
gcacagtacc tggaacagtc aagccctcaa taaatgttta ctgagtgcatt yaaaaaaaaa	681	
aaa	684	

<210> 292  
<211> 628  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 75..482

<221> sig\_peptide  
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<223> Von Heijne matrix  
score 3.5999990463257  
seq KMLISVAMLGAXA/GV

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<221> polyA_signal
<222> 595..600

<221> polyA_site
<222> 618..627

<400> 292
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ctgtgcaggc ggcc atg gat tcc ttg cgg aaa atg ctg atc tca gtc gca      110
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala
-15          -10
atg ctg ggc gca rgg gct ggc gtg ggc tac gcg ctc ctc gtt atc gtg      158
Met Leu Gly Ala Xaa Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val
-5           1           5           10
acc ccg gga gag cgg cgg aag cag gaa atg cta aag gag atg cca ctg      206
Thr Pro Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu
15           20           25
cag gac cca agg agc agg gag gac ggc agg acc cag cag cta ttg      254
Gln Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
30           35           40
ctg gcc act ctg cag gag gca gcg acc acg cag gag aac gtg gcc tgg      302
Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp
45           50           55
agg aag aac tgg atg gtt ggc ggc gaa ggc ggc gcc acg gga kgt cac      350
Arg Lys Asn Trp Met Val Gly Gly Glu Gly Ala Thr Gly Xaa His
60           65           70
cgt gag acc gga ctt gcc tcc gtg ggc ggc gga cct tgg ctt ggg cgc      398
Arg Glu Thr Gly Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg
75           80           85           90
agg aat ccg agg cag ctt tct cct tcg tgg gcc can cgg aaa atc cgg      446
Arg Asn Pro Arg Gln Leu Ser Pro Ser Trp Ala Xaa Arg Lys Ile Arg
95           100          105
amc gaa aat wcc atg cca gga ctc tcc ggg gtc ctg tgaactgccg      492
Xaa Glu Asn Xaa Met Pro Gly Leu Ser Gly Val Leu
110          115
tcgggtgagc acgtgtcccc caaacctgg actgactgct ttaaggtccg caaggcgggc      552
caggcccgag acgcgagtcg gatgtgttga actgaaagaaa ccaataaaat catgttcctc      612
cammcaaaaa aaaaah      628

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<210> 293
<211> 813
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 50..631

<221> sig_peptide
<222> 50..244
<223> Von Heijne matrix
      score 8
      seq LTLLGCLVTGVES/KI

<221> polyA_signal
<222> 777..782

<221> polyA_site
<222> 801..812

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<400> 293		58
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	-65	
gct ccc ctg agc tgc ctg tca ccg act aag tgg agc agt gtt tct tcc		106
Ala Pro Leu Ser Cys Leu Ser Pro Thr Lys Trp Ser Ser Val Ser Ser		
-60 -55 -50		
gca gac tca act gag aag tca gcc tct gcg gca ggc acc agg aat ctg		154
Ala Asp Ser Thr Glu Lys Ser Ala Ser Ala Ala Gly Thr Arg Asn Leu		
-45 -40 -35		
cct ttt cag ttc tgt ctc cggtt cag gct ttg agg atg aag gct gcg ggc		202
Pro Phe Gln Phe Cys Leu Arg Gln Ala Leu Arg Met Lys Ala Ala Gly		
-30 -25 -20 -15		
att ctg acc ctc att ggc tgc ctg gtc aca ggc gtc gag tcc aaa atc		250
Ile Leu Thr Leu Ile Gly Cys Leu Val Thr Gly Val Glu Ser Lys Ile		
-10 -5 1		
tac act cgt tgc aaa ctg gca aaa ata ttc tcg agg gct ggc ctg gac		298
Tyr Thr Arg Cys Lys Leu Ala Lys Ile Phe Ser Arg Ala Gly Leu Asp		
5 10 15		
aat cyg agg ggc ttc agc ctt gga aac tgg atc tgc atg gcg tat tat		346
Asn Xaa Arg Gly Phe Ser Leu Gly Asn Trp Ile Cys Met Ala Tyr Tyr		
20 25 30		
gag agc ggc tac aac acc aca gcc car acg gtc ctg gat gac ggc agc		394
Glu Ser Gly Tyr Asn Thr Thr Ala Gln Thr Val Leu Asp Asp Gly Ser		
35 40 45 50		
atc gac tay ggc atc ttc caa atc aac agc ttc gcg tgg tgc aga cgc		442
Ile Asp Tyr Gly Ile Phe Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg		
55 60 65		
gga aag ctg aag gag aac aac cac tgc cay gtc gcc tgc tca gcc ttg		490
Gly Lys Leu Lys Glu Asn Asn His Cys His Val Ala Cys Ser Ala Leu		
70 75 80		
rtc act gat gac ctc aca gat gca att atc tgt gcc arg aaa att gtt		538
Xaa Thr Asp Asp Leu Thr Asp Ala Ile Ile Cys Ala Xaa Lys Ile Val		
85 90 95		
aaa gag aca caa gga atg aac tat tgg caa ggc tgg aag aaa cay tgt		586
Lys Glu Thr Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys		
100 105 110		
gag ggg aga gac ctg tcc gas tgg aaa aaa ggc tgt gag gtt tcc		631
Glu Gly Arg Asp Leu Ser Xaa Trp Lys Lys Gly Cys Glu Val Ser		
115 120 125		
taaactggaa ctggacccag gatgcttcgc ascaacgccc tagggtttgc agtgaatgtc		691
caaatgcctg tgcatacttg tcccctttcc tcccaatatt ccttctcaaa cttggagagg		751
aaaaattaag ctataactttt aagaaaataa atatccat taaaatgtca amaaaaaaaaa		811
ah		813

<210> 294  
<211> 778  
<212> DNA  
<213> *Homo sapiens*

<220>  
<221> CDS  
<222> 154..576

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<221> sig_peptide
<222> 154..360
<223> Von Heijne matrix
      score 4.80000019073486
      seq MMVVLSLGII LASA/SF
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<221> polyA\_signal  
<222> 737..742

<221> polyA\_site  
<222> 763..775

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agtaaaaaaa cactggaata aggaaggcgt gatgacttc agaagatgaa ggtaagtaga	60		
aaccgttcat gggactgaga aaccagatgk aaaaccttt tggagcttc gaggactcg	120		
ctggAACCAA CGGGCACAGT tggcaacacc atc atg aca tca caa cct gtt ccc	174		
Met Thr Ser Gln Pro Val Pro			
-65			
aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa	222		
Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln			
-60	-55	-50	
gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa	270		
Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys			
-45	-40	-35	
cat cta cac gca gaa atc aaa gtt att ggg act atc cag atc ttg tgt	318		
His Leu His Ala Glu Ile Lys Val Ile Gly Thr Ile Gln Ile Leu Cys			
-30	-25	-20	-15
ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc	366		
Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe			
-10	-5	1	
tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac	414		
Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr			
5	10	15	
cca ttc ata gga ccc ttt ttt gtr akt aaa btt tct gag gag ggc agg	462		
Pro Phe Ile Gly Pro Phe Phe Val Xaa Lys Xaa Ser Glu Glu Gly Arg			
20	25	30	
atg ggg caa ara ggg gag gaa rat vcc aat agc tta aac ttc cca sct	510		
Met Gly Gln Xaa Gly Glu Glu Xaa Xaa Asn Ser Leu Asn Phe Pro Xaa			
35	40	45	50
gcc agc ttg cta tkt ttg atc tgc cag gav caa gga ttc aac ggt gaa	558		
Ala Ser Leu Leu Xaa Leu Ile Cys Gln Xaa Gln Gly Phe Asn Gly Glu			
55	60	65	
tct tgt tct cct gtc ggg targataaca ggggttgctt rattttagat	606		
Ser Cys Ser Pro Val Gly			
70			
caatttctta tcagactcaa ataaacattt ctttgaaaaa tcatcttatt ctgcacat	666		
tcatcttgag ctatgtgga aactagtgas ktctctccag gtttaggcga aaaaaaaaaatc	726		
catgaattag gataaagttg ggaaggaca tttatacaa aaaaaaaaaah cc	778		

<210> 295  
<211> 1060  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 154..897

<221> sig\_peptide  
<222> 154..360  
<223> Von Heijne matrix  
score 4.80000019073486  
seq MMVLSLGIILASA/SF

<221> polyA\_signal  
<222> 1017..1022

<221> polyA\_site  
<222> 1044..1054

<400> 295		
agaaaaaaaaa cactggaata aggaaggct gatgacttgc agaagatgaa ggttaagtaga	60	
aaccgttcat gggactgaga aaccagatgt aaaaccttt tggagcttct gaggactcag	120	
ctggAACCAA CGGGCACAGT TGGCAACACC ATC ATG ACA TCA CAA CCT GTT CCC	174	
Met Thr Ser Gln Pro Val Pro		
-65		
aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa	222	
Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln		
-60 -55 -50		
gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa	270	
Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys		
-45 -40 -35		
cac cta cac gca gar rtc aaa gtt att ggg act atc cag atc ttg tgt	318	
His Leu His Ala Glu Xaa Lys Val Ile Gly Thr Ile Gln Ile Leu Cys		
-30 -25 -20 -15		
ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc	366	
Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe		
-10 -5 1		
tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac	414	
Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr		
5 10 15		
cca ttc ata gga ccc ttt ttt atc atc tct ggc tct cta tca atc	462	
Pro Phe Ile Gly Pro Phe Phe Ile Ile Ser Gly Ser Leu Ser Ile		
20 25 30		
gcc aca aaa aaa agg tta acc aac ctt ttg gtg cat acc acc ctg gtt	510	
Ala Thr Lys Lys Arg Leu Thr Asn Leu Leu Val His Thr Thr Leu Val		
35 40 45 50		
gga agc att ctg agt gct ctg tct gcc ctg gtg ggt ttc att ayc ctg	558	
Gly Ser Ile Leu Ser Ala Leu Ser Ala Leu Val Gly Phe Ile Xaa Leu		
55 60 65		
tct gtc aaa cag gcc acc tta aat cct gcc tca ctg cak tgt gag ttg	606	
Ser Val Lys Gln Ala Thr Leu Asn Pro Ala Ser Leu Xaa Cys Glu Leu		
70 75 80		
gmc aaa aat aat ata cca aca ara akt tat gtt yct tac ttt tat cat	654	
Xaa Lys Asn Asn Ile Pro Thr Xaa Xaa Tyr Val Xaa Tyr Phe Tyr His		
85 90 95		
gat tca ctt tat acc acg gac kgc tat aca gcc aaa gcc akt ctg gct	702	
Asp Ser Leu Tyr Thr Asp Xaa Tyr Thr Ala Lys Ala Xaa Leu Ala		
100 105 110		
gga act ctc tct ctg atg ctg att tgc act ctg ctg gaa ttc tgc cwa	750	
Gly Thr Leu Ser Leu Met Leu Ile Cys Thr Leu Leu Glu Phe Cys Xaa		
115 120 125 130		
sct gtg ctc act gct gtg ctg cgg tgg aaa cag gct tac tct gac ttc	798	
Xaa Val Leu Thr Ala Val Leu Arg Trp Lys Gln Ala Tyr Ser Asp Phe		
135 140 145		
cct ggg agt gta ctt ttc ctg cct cam agt tac att ggw aat tct ggm	846	
Pro Gly Ser Val Leu Phe Leu Pro Xaa Ser Tyr Ile Gly Asn Ser Gly		
150 155 160		
atg tcc tca aaa atg acy cat gac tgt gga tat gaa gaa cta ttg act	894	
Met Ser Ser Lys Met Thr His Asp Cys Gly Tyr Glu Glu Leu Leu Thr		
165 170 175		
tct taagaaaaaaa gggagaaata ttaatcagaa agttgattct tatgataata	947	
Ser		
tggaaaagtt aaccattata gaaaagcaaa gcttgagttt cctaaatgta agcttttaaa	1007	
gtaatgaaca ttaaaaaaaaaa ccattatttc actgtcaaaa aaaaaamcc nkt	1060	

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<210> 296
<211> 444
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 146..292

<221> sig_peptide
<222> 146..253
<223> Von Heijne matrix
    score 5.5
    seq FTSMCILFHCLLS/FQ

<221> polyA_signal
<222> 395..400

<221> polyA_site
<222> 433..444

<400> 296
aacttgggac aagaratcaa actttaaaga tggcttaaag cccctttaa aggtctgact      60
gtgtcgacc tcttagagcta atctcaactag atgtgagcca ttgtttatat tctagccatc      120
ctttcatttc attctagaag acccc atg caa gtt ccc cac cta agg gtc tgg      172
                           Met Gln Val Pro His Leu Arg Val Trp
                           -35          -30
aca cag gtg awa gat acc ttc att ggt tat aga aat ttg gga ttt aca      220
Thr Gln Val Xaa Asp Thr Phe Ile Gly Tyr Arg Asn Leu Gly Phe Thr
   -25           -20          -15
agt atg tgc ata ttg ttc cac tgt ctt agc ttt cag gtt ttc aaa      268
Ser Met Cys Ile Leu Phe His Cys Leu Leu Ser Phe Gln Val Phe Lys
   -10           -5            1            5
aag aaa aga aaa ctt ara ctt ttc tgatgttctt tttacgtaa ataaccattt      322
Lys Lys Arg Lys Leu Xaa Leu Phe
   10
tatttgttggc ttgtttttc tgccttcaaa ctactccac aggc当地 aata tavctggctg      382
cttcttctg taaataaaagt ttatggc cacagccatg gccatcttt aaaaaaaaaa      442
aa
   444

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<210> 297
<211> 754
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 126..383

<221> sig_peptide
<222> 126..167
<223> Von Heijne matrix
    score 7.5
    seq VALNLILVPCCAA/WC

<221> polyA_signal
<222> 726..731

<221> polyA_site
<222> 743..754

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<400> 297  
 aattgtatgt tacgatgtt tattgatttt taagaaagta attkratgg taaaacttct 60  
 gctcgttac actgcacatt gaatacaggt aactaattgg wwggagaggg gaggtcaactc 120  
 ttttg atg gtg gcc ctg aac ctc att ctg gtt ccc tgc tgc gct gct tgg 170  
 Met Val Ala Leu Asn Leu Ile Leu Val Pro Cys Cys Ala Ala Trp  
 -10 -5 1  
 tgt gac cca cgg agg atc cac tcc cag gat gac gtg ctc cgt agc tct 218  
 Cys Asp Pro Arg Arg Ile His Ser Gln Asp Asp Val Leu Arg Ser Ser  
 5 10 15  
 gct gct gat act ggg tct gcg atg cag cgg cgt gag gcc tgg gct ggt 266  
 Ala Ala Asp Thr Gly Ser Ala Met Gln Arg Arg Glu Ala Trp Ala Gly  
 20 25 30  
 tgg aga agg tca caa ccc ttc tct gtt ggt ctg cct tct gct gaa aga 314  
 Trp Arg Arg Ser Gln Pro Phe Ser Val Gly Leu Pro Ser Ala Glu Arg  
 35 40 45  
 ctc gag aac caa cca ggg aag ctg tcc tgg agg tcc ctg gtc gga gag 362  
 Leu Glu Asn Gln Pro Gly Lys Leu Ser Trp Arg Ser Leu Val Gly Glu  
 50 55 60 65  
 gga cat aga atc tgt gac ctc tgacrrctgt gaasccaccc tgggctacar 413  
 Gly His Arg Ile Cys Asp Leu  
 70  
 aaaccacagt cttcccagca attattacaa ttcttgaatt ccttgggat ttttactgc 473  
 ccttcaaag cacttaaktg tkrratctaa cgkttccag tgtctgtctg aggtgactta 533  
 aaaaatcaga acaaaaacttc tattatccag agtcatggga gagtacaccc tttccaggaa 593  
 taatgttttggaaacactg aaatgaaatc ttcccagtagtataaatttgt gtataaaaa 653  
 aaaagaaaact tttctgaatg cctacctggc ggtgtataacc aggcagtgtg ccagttaaa 713  
 aagatgaaaa agaataaaaaa ctttgagga aaaaaaaaaa a 754

<210> 298  
<211> 629  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> CDS  
<222> 66..497  
  
<221> sig\_peptide  
<222> 66..239  
<223> Von Heijne matrix  
 score 5.40000009536743  
 seq QLDSLWLGALG/LT  
  
<221> polyA\_signal  
<222> 594..599  
  
<221> polyA\_site  
<222> 618..629  
  
<400> 298  
 aactcccaga atgctgacca aagtgggagg agcacttaggt cttcccgta cctccaccc 60  
 tctcc atg acc cgg ctc tgc tta ccc aga ccc gaa gca cgt gag gat ccg 110  
 Met Thr Arg Leu Cys Leu Pro Arg Pro Glu Ala Arg Glu Asp Pro  
 -55 -50 -45  
 atc cca gtt cct cca agg ggc ctg ggt gct ggg gag ggg tca ggt agt 158  
 Ile Pro Val Pro Pro Arg Gly Leu Gly Ala Gly Glu Gly Ser Gly Ser  
 -40 -35 -30  
 cca gtg cgt cca cct gta tcc acc tgg ggc cct agc tgg gcc cag ctc 206  
 Pro Val Arg Pro Pro Val Ser Thr Trp Gly Pro Ser Trp Ala Gln Leu

-25	-20	-15	
ctg gac agt gtc cta tgg ctg ggg gca cta gga ctg aca atc cag gca			254
Leu Asp Ser Val Leu Trp Leu Gly Ala Leu Gly Leu Thr Ile Gln Ala			
-10	-5	1	5
gtc ttt tcc acc act ggc cca gcc ctg ctg ctt ctg gtc agc ttc			302
Val Phe Ser Thr Thr Gly Pro Ala Leu Leu Leu Leu Val Ser Phe			
10	15	20	
ctc acc ttt gac ctc cat agg ccc gca gtc aca ctc tgc cac agc			350
Leu Thr Phe Asp Leu Leu His Arg Pro Ala Val Thr Leu Cys His Ser			
25	30	35	
gca aac ttc tca cca ggg gcc aga gtc agg ggg ccg gtg aag gtc ctg			398
Ala Asn Phe Ser Pro Gly Ala Arg Val Arg Gly Pro Val Lys Val Leu			
40	45	50	
gac agc agg agg ctc tac tcc tgc aaa tgg gta cag tct cag gac aac			446
Asp Ser Arg Arg Leu Tyr Ser Cys Lys Trp Val Gln Ser Gln Asp Asn			
55	60	65	
tta gcc tcc agg aag cac tgc tgc tgc tca tgg ggc tgg gcc cgc			494
Leu Ala Ser Arg Lys His Cys Cys Cys Ser Trp Gly Trp Ala Arg			
70	75	80	85
tcc tgaaaacctg tggcatgccc ttgwaccctg cttggcctgg ctttctgcct			547
Ser			
ccatccttgg gcctgakanc ccctccccac aactcagtgt cttcaaata tacaatgacc			607
acccttcttc aaaaaaaaaaa aa			629

<210> 299  
<211> 765  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 49..411

<221> sig\_peptide  
<222> 49..96  
<223> Von Heijne matrix  
score 10.1000003814697  
seq LVLTLC TLPLAVA/SA

<221> polyA\_signal  
<222> 732..737

<221> polyA\_site  
<222> 750..763

<400> 299  
aaagatccct gcagccccggc aggagagaag gctgagcctt ctggcgtc atg gag agg  
Met Glu Arg  
-15

ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc  
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly  
-10 -5 1  
tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag  
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys  
5 10 15  
gtc agc agc tgg acg gag tgc ccg acc tgg tgc agc ccg ctg gac  
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp  
20 25 30 35  
caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt agt gag tcy ccc  
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Ser Glu Ser Pro  
249

40	45	50	
ccg ggc aga ggg cas gtg cca bgt gcc ggg gaa kgg ccg gtg ccc ccg			
Pro Gly Arg Gly Xaa Val Pro Xaa Ala Gly Glu Xaa Pro Val Pro Pro			
55	60	65	
cct ctc wkc gac tta bct atg act cct cgg ckc ycc agg gcc tgg ggc			
Pro Leu Xaa Asp Leu Xaa Met Thr Pro Arg Xaa Xaa Arg Ala Trp Gly			
70	75	80	
cck gtg ggt ccd aaa gtg cct cct gct gtc tct ccc gcg ctg ggc tcg			
Pro Val Gly Pro Lys Val Pro Pro Ala Val Ser Pro Ala Leu Gly Ser			
85	90	95	
ggc gag cat ccs rva btg tgaatkkkga ctttttctc ckccatttga			
Gly Glu His Pro Xaa Xaa			
100	105		
agtgtcacta ggaactgtca gcaggacaaa ggctctgatg tcactgaatt tacaaaraca			501
gcaggaacrs ackgggtgggg atgggcagct gttcrargcr atgggtkac tgccttcct			561
ggcacagcac artacacacctg ccataacaacc carcatcagg cakgctgcac tggaatcgat			621
acagtgtatg acaatgtcat atagtataac acaaataat gaatataacg tgtatattgc			681
aacttaatat aatacgtatg aatataatgc tacataatac aacataataat aataaaatag			741
aatgcaacac aaaaaaaaaa aacc			765

<210> 300  
<211> 623  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 49..534

<221> sig\_peptide  
<222> 49..96  
<223> Von Heijne matrix  
score 10.1000003814697  
seq LVLTLC TLPLAVA/SA

<221> polyA\_signal  
<222> 593..598

<221> polyA\_site  
<222> 612..623

<400> 300  
aaagatccct gcagccccgc aggagagaag gctgagccctt ctggcgtc atg gag agg  
Met Glu Arg  
-15

-10	-5	1
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ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc  
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly

5	10	15
---	----	----

tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag  
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys

20	25	30	35
----	----	----	----

gtc agc agc tgg acg gag tgc ccg ccc acc tgg tgc agc ccg ctg gac  
Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp

40	45	50
----	----	----

caa gtc tgc atc tcc aac gag gtg gtc gtc tct ttt aaa tgg agt gta  
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys Trp Ser Val

55	60	65
----	----	----

cgc gtc ctg ctc agc aaa cgc tgt gct ccc aga tgt ccc aac gac aac  
Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Asp Asn

atg aak ttc gaa tgg tcg ccg gcc ccc atg gtg caa ggc gtg atc acc Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly Val Ile Thr 70 75 80	345
agg cgc tgc tgt tcc tgg gct ctc tgc aac agg gca ctg acc cca cag Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu Thr Pro Gln 85 90 95	393
gag ggg cgc tgg gcc ctg cra ggg ggg ctc ctg ctc cag gac cct tcg Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Gln Asp Pro Ser 100 105 110 115	441
agg ggc ara aaa acc tgg gtg cgg cca cag ctg ggg ctc cca ctc tgc Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu Pro Leu Cys 120 125 130	489
ctt ccc awt tcc aac ccc ctc tgc cca rgg gaa acc cag gaa gga Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln Glu Gly 135 140 145	534
taacactgtg ggtgccccca cctgtgcatt gggaccacra cttcacccctc ttggaracaa taaactctca tgcccccaaa aaaaaaaaa	594 623

<210> 301  
<211> 571  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 86..415

<221> sig\_peptide  
<222> 86..145  
<223> Von Heijne matrix  
score 9.80000019073486  
seq FTIGLTLLGXQA/MP

<221> polyA\_signal  
<222> 540..545

<221> polyA\_site  
<222> 560..571

<400> 301 aaaaactcac ccagttagtg tgagcattta agaagcatcc tctgccaaga ccaaaaggaa agaagaaaaa bggccaaaag caaaa atg ara ctg atg gta ctt gtt ttc acc Met Xaa Leu Met Val Leu Val Phe Thr -20 -15	60 112
att ggg cta act ttg ctg cta gga rtt caa gcc atg cct gca aat cgc Ile Gly Leu Thr Leu Leu Gly Xaa Gln Ala Met Pro Ala Asn Arg -10 -5 1 5	160
ctc tct tgc tac aga aag ata cta aaa gat cac aac tgt cac aac ctt Leu Ser Cys Tyr Arg Lys Ile Leu Lys Asp His Asn Cys His Asn Leu 10 15 20	208
ccg gaa gga gta gct gac ctg aca cag att gat gtc aat gtc cag gat Pro Glu Gly Val Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp 25 30 35	256
cat ttc tgg gat ggg aag gga tgt gag atg atc tgt tac tgc aac ttc His Phe Trp Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe 40 45 50	304
aag cga att gct ctg ctg ccc aaa aga cgt ttt ctt tgg acc aaa gat Lys Arg Ile Ala Leu Leu Pro Lys Arg Arg Phe Leu Trp Thr Lys Asp 55 60 65	352
ctc ttt cgt gat tcc ttg caa caa tca atg aga atc ttc atg tat tct	400

Leu Phe Arg Asp Ser	Leu Gln Gln Ser Met Arg Ile Phe Met Tyr Ser		
70	75	80	85
ggc gaa cac cat tcc	tgatccc caaactgcac tacatcgta taactgcatt		455
Gly Glu His His Ser			
90			
tctagttct atatagtgcata atagagcata gattctataa attcttactt gtctaagaaa		515	
gttaaatctgt gttaaacaag tagtaataaa agttaattca atccaaaaaa aaaaaaa		571	

<210> 302  
<211> 612  
<212> DNA  
<213> Homo sapien

<220>  
<221> CDS  
<222> 56..268

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<221> sig_peptide
<222> 56..100
<223> Von Heijne matrix
      score 4.59999990463257
      seq LLTHNLLSSHVRG/VG
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<221> polyA\_signal  
<222> 584..589

<221> polyA\_site  
<222> 601..612

<400> 302  
ctaatcgaaa agggggattt tccgggttcgg gcctggcgag agtttgtgcg gcgac atg 58  
Met  
-15

aaa ctg ctt acc cac aat ctg ctg agc tcg cat gtg cg<sub>g</sub> ggg gtg ggg  
 Lys Leu Leu Thr His Asn Leu Leu Ser Ser His Val Arg Gly Val Gly  
           10          25          35

-10            -5            1

tcc cgt ggc ttc ccc ctg cgc ctc cag gcc acc gag gtc cgt atc tgc	154
Ser Arg Gly Phe Pro Leu Arg Leu Gln Ala Thr Glu Val Val Arg Ile Cys	

5	10	15	
cct gtg gaa ttc aac ccc aac ttc gtg gcg cgt atg ata cct aaa gtg			202
Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys Val			:
20	25	30	

gag tgg tcg gcg ttc ctg gag gcg rmc gat aac ttg cgt ctg atc cag  
 Glu Trp Ser Ala Phe Leu Glu Ala Xaa Asp Asn Leu Arg Leu Ile Gln  
 35 40 45 50

gtg ccg aga agg gcc ggt tgagggatat gaggagaatg aggagttct 298  
Val Pro Arg Arg Ala Gly

55		
gaggaccatg caccacactgc tgctggaggt ggamstgaka gagggcaccc tgcagtgcc	358	
ggaatctgga cgtatgttcc ccatcagccg cgggatcccc aacatgctgc tgagtgaaga	418	
ggaaactgag agttgattgt gccaggcgcc agttttctt gttatgactg tgtattttg	478	
ttgatctata ccctgtttcc gaattctgcc gtgtgtatcc ccaacccttg acccaatgac	538	
accaaacaca gtgttttga gtcggattt atatatttt ttctcattaa aggtttaaaa	598	
ccaaaaaaaaaaa aaaa	612	

<210> 303  
<211> 539  
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 32..328

<221> sig\_peptide

<222> 32..103

<223> Von Heijne matrix

score 4.59999990463257

seq FFIFCSLNTLLLGV/GV

<221> polyA\_signal

<222> 508..513

<221> polyA\_site

<222> 528..539

<400> 303

aacaactatc ctgcctgtcg cttgctgcac c atg aag tct gcc aag ctg gga	52		
Met Lys Ser Ala Lys Leu Gly			
-20			
ttt ctt cta aga ttc atc ttc tgc tca ttg aat acc ctg tta ttg	100		
Phe Leu Leu Arg Phe Phe Ile Phe Cys Ser Leu Asn Thr Leu Leu Leu			
-15	-10	-5	
ggt ggt gtt aat aaa att gcg gag aag ata tgt gga gac ctc aaa gat	148		
Gly Gly Val Asn Lys Ile Ala Glu Lys Ile Cys Gly Asp Leu Lys Asp			
1	5	10	15
ccc tgc aaa ttg gac atg aat ttt gga agc tgc tat gaa gtt cac ttt	196		
Pro Cys Lys Leu Asp Met Asn Phe Gly Ser Cys Tyr Glu Val His Phe			
20	25	30	
aga tat ttc tac aac aga acc tcc aaa aga tgt gaa act ttt gtc ttc	244		
Arg Tyr Phe Tyr Asn Arg Thr Ser Lys Arg Cys Glu Thr Phe Val Phe			
35	40	45	
tcc agc tgt aat ggc aac ctt aac aac ttc aag ctt aaa ata gaa cgt	292		
Ser Ser Cys Asn Gly Asn Leu Asn Asn Phe Lys Leu Lys Ile Glu Arg			
50	55	60	
gaa gta kcc tgt gtt gca aaa tac aaa cca ccg agg tgagaggatg	338		
Glu Val Xaa Cys Val Ala Lys Tyr Lys Pro Pro Arg			
65	70	75	
tgaactcatg aagttgtctg ctgcaccatc cgaaataaa acacaagaaa attcaractg	398		
atttwgaat ctttgttwta tttccmymak ggcgwktaag cttccatatg tttgctat	458		
tcctgaccct agtttgtct ttcttgaaa ttaactgtat gakcattasa atgaaagagt	518		
ctttctgtca aaaaaaaaaa a	539		

<210> 304

<211> 964

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 21..527

<221> sig\_peptide

<222> 21..95

<223> Von Heijne matrix

score 8.5

seq LKVLLLPLAPAAA/QD

<221> polyA\_signal  
<222> 921..926

<221> polyA\_site  
<222> 953..963

<400> 304

agggcgatc ttctccggcc atg agg aag cca gcc gct ggc ttc ctt ccc tca Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser	-25	-20	-15	53
ctc ctg aag gtg ctg ctc ctg cct ctg gca cct gcc gca gcc cag gat Leu Leu Lys Val Leu Leu Pro Leu Ala Pro Ala Ala Gln Asp	-10	-5	1	101
tcg act cag gcc tcc act cca ggc agc cct ctc tct cct acc gaa tac Ser Thr Gln Ala Ser Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr	5	10	15	149
caa cgcc ttc ttc gca ctg ctg act cca acc tgg aag gca gar act acc Gln Arg Phe Phe Ala Leu Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr	20	25	30	197
tgc cgt ctc cgt gca acc cac ggc tgc cgg aat ccc aca ctc gtc cag Cys Arg Leu Arg Ala Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln	35	40	45	245
ctg gac caa tat gaa aac cac ggc tta gtg ccc gat ggt gct gtc tgc Leu Asp Gln Tyr Glu Asn His Gly Leu Val Pro Asp Gly Ala Val Cys	55	60	65	293
tcc aac ctc cct tat gcc tcc tgg ttt gag tct ttc tgc cag ttc act Ser Asn Leu Pro Tyr Ala Ser Trp Phe Glu Ser Phe Cys Gln Phe Thr	70	75	80	341
cac tac cgt tgc tcc aac cac gtc tac tat gcc aag aga gtc ctg tgt His Tyr Arg Cys Ser Asn His Val Tyr Tyr Ala Lys Arg Val Leu Cys	85	90	95	389
tcc cag cca gtc tct att ctc tcw cct aac act ctc aag gag ata gaa Ser Gln Pro Val Ser Ile Leu Ser Pro Asn Thr Leu Lys Glu Ile Glu	100	105	110	437
sct tca gct gaa gtc tca ccc acc aca gat gac ctc ccc cat ctc acc Xaa Ser Ala Glu Val Ser Pro Thr Thr Asp Asp Leu Pro His Leu Thr	115	120	125	485
cca ctt cac agt gac aga acg cca gac ctt cca gcc ctg gcc Pro Leu His Ser Asp Arg Thr Pro Asp Leu Pro Ala Leu Ala	135	140	130	527
tgagaggctc agcaacaacg tggaagagct cctacaatcc tccttgtccc tgggaggccca ggagcaagcg ccagagcaca agcaggagca aggagtggag cacaggcagg agccgacaca				587
agaacacaag caggaagagg ggcagaaaca ggaagagcaa gaagaggaac aggaagagga				647
gggaaagcag gaagaaggac agggactaa ggagggacgg gaggtctgtgt ctcagctgca				707
gacagactca gagcccaagt ttcaactctga atctctatct tctaaccctt cctctttgc				767
tccccggta cganaagtag agtctactcc tatgataatg gagaacatcc aggagctcat				827
tcgatcagcc cagaaatag atgaaatgaa tgaaatatat gatgagaact cctactggag				887
aaacccaaaa aaaaaak				947
				964

<210> 305

<211> 684

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 147, .647

<221> sig peptide

<222> 147, .374

<223> Von Heijne matrix  
score 3.5  
seq LASASELPLGSRP/AP

<221> polyA\_site  
<222> 668..681

<400> 305

aaccttctgt gagcccccggcg gtgacaacgg caacatggcc cgtgaacgga gctgaagtcg acgacttctc ctrgrarmcc ccgactgagg cgagacgaa ggtgctgcag gcgcgacggg agcggcaaga tcgcattc cggctc atg ggc gac tat ctg ctg cgc ggt tac	60 120 173		
Met Gly Asp Tyr Leu Leu Arg Gly Tyr			
-75	-70		
cgc atg ctg ggc gag acg tgc gac tgc ggg acg atc ctc ctc caa Arg Met Leu Gly Glu Thr Cys Ala Asp Cys Gly Thr Ile Leu Leu Gln	221		
-65	-60	-55	
gac aaa cag .cgg aaa atc tac tgc gtg gct tgc cag gaa ctc gac tca Asp Lys Gln Arg Lys Ile Tyr Cys Val Ala Cys Gln Glu Leu Asp Ser	269		
-50	-45	-40	
gac gtg gat aaa gat aat ccc gct ctg aat gcc cag gct gcc ctc tcc Asp Val Asp Lys Asp Asn Pro Ala Leu Asn Ala Gln Ala Ala Leu Ser	317		
-35	-30	-25	-20
caa gct cgg gag cac cag ctg gcc tca gcc tca gag ctc ccc ctg ggc Gln Ala Arg Glu His Gln Leu Ala Ser Ala Ser Glu Leu Pro Leu Gly	365		
-15	-10	-5	
tct cga cct gcg ccc caa ccc cca gta cct cgt ccg gag cac tgt gag Ser Arg Pro Ala Pro Gln Pro Pro Val Pro Arg Pro Glu His Cys Glu	413		
1	5	10	
gga gct gca gca gga ctc aag gca gcc cag ggg .cca cct gct cct gct Gly Ala Ala Ala Gly Leu Lys Ala Ala Gln Gly Pro Pro Ala Pro Ala	461		
15	20	25	
gtg cct cca aat aca rat gtc atg gcc tgc aca cag aca gcc ctc ttg Val Pro Pro Asn Thr Xaa Val Met Ala Cys Thr Gln Thr Ala Leu Leu	509		
30	35	40	45
caa aag ctg acc tgg gcc tct gct gaa ctg ggc tct anc acc tcc cyg Gln Lys Leu Thr Trp Ala Ser Ala Glu Leu Gly Ser Xaa Thr Ser Xaa	557		
50	55	60	
gga aaa mta gca tcc agc tgc gtc gtc tcc tcc gcg cat gtg cgg agg Gly Lys Xaa Ala Ser Ser Cys Val Ala Leu Ser Ala His Val Arg Arg	605		
65	70	75	
ccc tgc gca gcc tgc agc agc tac agc act aag aga agc ccc Pro Cys Ala Ala Cys Ser Ser Tyr Ser Thr Lys Arg Ser Pro	647		
80	85	90	
tgagaaaaaac ctcttagaaaaa acaaaaaaaaaaaa aaaaccc	684		

<210> 306  
<211> 693  
<212> DNA  
<213> *Homo sapiens*

<220>  
<221> CDS  
<222> 262..471

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<221> sig_peptide
<222> 262..306
<223> Von Heijne matrix
      score 3.5
      seq LCFLLPHHRLQEA/RQ
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<221> polyA\_signal  
<222> 663..668

<221> polyA\_site  
<222> 682..693

<400> 306

atttcgccgc gctcgcbgma cyhsgwtgtt cagcaccctc ggtccgggttg aggttgtcaa	60
gtcggmccaa acagggttgtt tctctgcagt ttccaacatg gcagggmsgt ttaatagaca	120
tggataagaa gtccactcac agaaatcctg aagatgccag ggctggcaaa tatgaaggtt	180
aacacaaaacg aaagaaaaaga agaaagcaaa accaaaacca gcaccgatcc cgacatagat	240
cagtgacgtc ttttcttca g atg atc cta tgt ttc ctt ctt cct cat cat	291
Met Ile Leu Cys Phe Leu Leu Pro His His	
-15 -10	
cgt ctt cag gaa gcc aga cag att caa gta ttg aag atg ctt cca agg	339
Arg Leu Gln Glu Ala Arg Gln Ile Gln Val Leu Lys Met Leu Pro Arg	
-5 1 5 10	
gaa aaa tta aga aga aga gaa gag aga aaa caa ata aat ggg aaa aaa	387
Glu Lys Leu Arg Arg Glu Glu Arg Lys Gln Ile Asn Gly Lys Lys	
15 20 25	
raa agg aca aaa tat gaa aca cca aga aaa rga raa gga aaa aaa gga	435
Xaa Arg Thr Lys Tyr Glu Thr Pro Arg Lys Xaa Xaa Gly Lys Lys Gly	
30 35 40	
gga aac mac cmc wtw tkt cmc ctt tcc aar agg gac tgaaactggg	481
Gly Asn Xaa Xaa Xaa Xaa Leu Ser Lys Arg Asp	
45 50 55	
ctgacccttt tgatttccaa vctcascgtt ttgggtgttaag gcggccaaar aaggatgcgg	541
ascccagcac tgtgaagcct acaaaaaacat tgatgcgcgtg gcttggggat ttgaatttga	601
acatcttca cactaagttc agactcatga aaccaatctt cagatgctct gtaaaaccaca	661
taataaaagag ttggaaatt aaaaaaaaaaar aa	693

<210> 307  
<211> 1656  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 74..1216

<221> sig\_peptide  
<222> 74..172  
<223> Von Heijne matrix  
score 5.80000019073486  
seq XLCLGMALCPRQA/TR

<221> polyA\_signal  
<222> 1627..1632

<221> polyA\_site  
<222> 1640..1652

<400> 307

atctcttggc gtctcaacgt tcggatcagc agctttttc cattctctct ctccacttct	60
tcagtgagca gcc atg agt tgg act gtg cct gtt gtg cgg gcc agc cag	109
Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln	
-30 -25	
aga gtg agc tcg gtg gga gcg aat ktc cta tgc ctg ggg atg gcc ctg	157
Arg Val Ser Ser Val Gly Ala Asn Xaa Leu Cys Leu Gly Met Ala Leu	
-20 -15 -10	

tgt ccg cgt caa gca acg cgc atc ccg ctc aac ggc acc tgg ctc ttc	205
Cys Pro Arg Gln Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe	
-5 1 5 10	
acc ccc gtg agc aag atg gcg act gtg aar agt gag ctt att gag cgt	253
Thr Pro Val Ser Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg	
15 20 25	
tcc act tcc gar aag ccc gtt cat cac agt aag gtc tcc atc ata gga	301
Phe Thr Ser Glu Lys Pro Val His His Ser Lys Val Ser Ile Ile Gly	
30 35 40	
act gga tcg gtg ggc atg gcc tgc gct atc agc atc tta tta aaa ggc	349
Thr Gly Ser Val Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly	
45 50 55	
ttg agt gat gaa ctt gcc ctt gtg gat ctt gat gaa rac aaa ctg aag	397
Leu Ser Asp Glu Leu Ala Leu Val Asp Leu Asp Glu Xaa Lys Leu Lys	
60 65 70 75	
ggg gag acr atg gat ctt caa cat ggc agc cct ttc acg aaa atg cca	445
Gly Glu Thr Met Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro	
80 85 90	
aat att gtt tgt agc aaa rat tac ttt gtc aca gca aac tcc aac cta	493
Asn Ile Val Cys Ser Lys Xaa Tyr Phe Val Thr Ala Asn Ser Asn Leu	
95 100 105	
gtg att atc aca gca ggt gca cgc caa raa aag gga gaa acg cgc ctt	541
Val Ile Ile Thr Ala Gly Ala Arg Gln Xaa Lys Gly Glu Thr Arg Leu	
110 115 120	
aat tta stc cag cga aat gtg gcc atc ttc aag tta atg att tcc agt	589
Asn Leu Xaa Gln Arg Asn Val Ala Ile Phe Lys Leu Met Ile Ser Ser	
125 130 135	
att gtc cag tac agc ccc cac tgc aaa ctg att att gtt tcc aat cca	637
Ile Val Gln Tyr Ser Pro His Cys Lys Leu Ile Ile Val Ser Asn Pro	
140 145 150 155	
gtg gat atc tta act tat gta gct tgg aag ttg agt gca ttt ccc aaa	685
Val Asp Ile Leu Thr Tyr Val Ala Trp Lys Leu Ser Ala Phe Pro Lys	
160 165 170	
aac cgt att att gga agc ggc tgt aat ctg ata mhg gct cgt ttt cgt	733
Asn Arg Ile Ile Gly Ser Gly Cys Asn Leu Ile Xaa Ala Arg Phe Arg	
175 180 185	
tcc ttg att gga caa aag ctt ggt atc cat tct gaa agc tgc cat gga	781
Phe Leu Ile Gly Gln Lys Leu Gly Ile His Ser Glu Ser Cys His Gly	
190 195 200	
tgg atc ctc gga gag cat gga gac tca agt gtt cct gtg tgg agt gga	829
Trp Ile Leu Gly Glu His Gly Asp Ser Ser Val Pro Val Trp Ser Gly	
205 210 215	
gtg aac ata gct ggt gtc cct ttg aag gat ctg aac tct gat ata gga	877
Val Asn Ile Ala Gly Val Pro Leu Lys Asp Leu Asn Ser Asp Ile Gly	
220 225 230 235	
act gat aaa gat cct gag caa tgg aaa aat gtc cac aaa gaa gtg act	925
Thr Asp Lys Asp Pro Glu Gln Trp Lys Asn Val His Lys Glu Val Thr	
240 245 250	
gca act gcc tat gag att att aaa atg aaa ggt tat act tct tgg gcc	973
Ala Thr Ala Tyr Glu Ile Ile Lys Met Lys Gly Tyr Thr Ser Trp Ala	
255 260 265	
att ggc cta tct gtg gcc gat tta aca gaa agt att ttg aag aat ctt	1021
Ile Gly Leu Ser Val Ala Asp Leu Thr Glu Ser Ile Leu Lys Asn Leu	
270 275 280	
agg aga ata cat cca gtt tcc acc ata act aag ggc ctc tat gga ata	1069
Arg Arg Ile His Pro Val Ser Thr Ile Thr Lys Gly Leu Tyr Gly Ile	
285 290 295	
rat gaa gaa gta ttc ctc agt att cct tgt atc ctg gga gag aac ggt	1117
Xaa Glu Glu Val Phe Leu Ser Ile Pro Cys Ile Leu Gly Glu Asn Gly	
300 305 310 315	
att acc aac ctt ata aag ata aag ctg acc cct gaa gaa gag gcc cat	1165
Ile Thr Asn Leu Ile Lys Ile Lys Leu Thr Pro Glu Glu Ala His	

320	325	330	
ctg aaa aaa agt gca aaa aca ctc tgg gaa att cag aat aag ctt aag			1213
Leu Lys Lys Ser Ala Lys Thr Leu Trp Glu Ile Gln Asn Lys Leu Lys			
335	340	345	
ctt taaagttgcc taaaactacc attccgaaat tattgaagag atcatagata			1266
Leu			
caggattata taacgaaatt ttgaataaac ttgaattcct aaaagatgga aacaggaaag			1326
taggttaggt gatttccta ttatattgt cctccagctc ttttattgag catccacgtg			1386
ctggacgata ctatattaca attcckaagt atttttggta cctctgtatgt agcagcactt			1446
gcacatgttat atatatgttag ttgrmatgg gttccaaaa agtaggatgt aggtatttat			1506
tgtgttctag aaattccgac tcttttcatt agatatatgc tattttttc atttttgctg			1566
gtttataacct atgttcatat atatgtgtaa aaaaagtagt agcttcttct acaatgtaaa			1626
aataaatgtaa catacaaaaaa aaaaaamcmc			1656

<210> 308  
<211> 517  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 48..164

<221> sig\_peptide  
<222> 48..89  
<223> Von Heijne matrix  
score 4  
seq YYMVCLFFRLIFs/EH

<221> polyA\_signal  
<222> 482..487

<221> polyA\_site  
<222> 505..517

<400> 308			
aggagatagc ctcgtagaaa tgacaaccac aatgttaata ctaacat atg tat tac			56
		Met Tyr Tyr	
atg gtt tgt ttg ttc ttt cgc tta ata ttt tca gag cac cta cct att			104
Met Val Cys Leu Phe Phe Arg Leu Ile Phe Ser Glu His Leu Pro Ile			
-10	-5	1	5
ata ggc act gtc act tct cac aaa act ggg aca cta act gtt tat cca			152
Ile Gly Thr Val Thr Ser His Lys Thr Gly Thr Leu Thr Val Tyr Pro			
10	15	20	
aca tct gct ggc taaataaaga catgatcttc acctttggg attgttaatt			204
Thr Ser Ala Gly			
25			
taaaatgggtt ccataagagc aatgcaaaga cagagatatt tggcagcact gcagctggtg			264
atttatatgg ctcttcacaa ggtgttattt tgggttatca aggtatggat gcttaaatca			324
gctgcaggaa gtaagaaaga agaaaaaaaaa agtgataaaag ataaaaaaaaa atcaaccttg			384
gtccttccac caaaacccat taatttccat atcatcatct gcataararg gaaaattcct			444
acwtgaccag gttactgcaa ggatktkaat tttgaatatt aaaatattat mcmcaattgg			504
aaaaaaaaaaa aaa			517

<210> 309  
<211> 405  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 185..334

<221> sig\_peptide  
<222> 185..295  
<223> Von Heijne matrix  
score 5.90000009536743  
seq LSYASSALSPCLT/AP

<221> polyA\_signal  
<222> 355..360

<221> polyA\_site  
<222> 392..405

<400> 309

atcaccttct tctccatcct tstctgggcc agtccccarc ccagtcctc tcctgacctg	60	
cccagcccaa gtcagccttc agcacgcgtc ttctgcaca cagatattcc aggctact	120	
ggcatccag gaccccgma atgatgcctc agtcccttac aagcgcttcc tggatgaggg	180	
tggc atg gtg ctg acc acc ctc ccc ttg ccc tct gcc aac agc cct gtg	229	
Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val		
-35	-30	-25
aac atg ccc acc act ggc ccc aac agc ctg agt tat gct agc tct gcc	277	
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala		
-20	-15	-10
ctg tcc ccc tgt ctg acc gct cca aag tcc ccc cga ctt gct atg atg	325	
Leu Ser Pro Cys Leu Thr Ala Pro Lys Ser Pro Arg Leu Ala Met Met		
-5	1	5
cct gac aac taaatatcct tatccaaatc aataaarwra raatcctccc	374	
Pro Asp Asn		
tccaraaggg tttctaaaaa caaaaaaaaaa a	405	

<210> 310  
<211> 1087  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> 195..347

<221> sig\_peptide  
<222> 195..272  
<223> Von Heijne matrix  
score 7.09999990463257  
seq LASLQWSLTLAWC/GS

<221> polyA\_signal  
<222> 1037..1042

<221> polyA\_site  
<222> 1071..1082

<400> 310

aaagtgtaga acacggacct ctgagttatg ctcttgagag gtgccaaagc tgggctgttt	60
acctaccta tccacagagc tctgaaagtc aagccagaaa ggaaggattc caaattcttg	120
gaattttatc tagaaaagaa gactaagcag cttttgttct tctgtgaccc agttgctggc	180
ccaagacatg gaca atg acc ccc tgg tgt ttg gcg tgt ctg ggg agg agg	230